

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 17, 2006, 15:33:18 ; Search time 1.8328 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88

Sequence: 1 ELSEGISAINRMIGVGLV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	90.9	370	2	A49528
2	46	52.3	603	1	YUBHY
3	46	52.3	605	1	S07314
4	46	52.3	608	2	T14731
5	46	52.3	609	2	J00703
6	46	52.3	609	2	S11481
7	46	52.3	615	1	YUWY
8	45	51.1	332	2	T36741
9	45	51.1	368	2	S75652
10	44	50.0	394	2	S75652
11	43	48.9	90	2	A23735
12	43	48.9	90	2	S15095
13	43	48.9	259	2	A87377
14	43	48.9	3076	2	A87058
15	42	47.7	422	1	JGAGLR
16	42	47.7	506	2	D54190
17	42	47.7	699	2	D70667
18	41.5	47.2	495	1	S14384
19	41	46.6	80	1	ZABP74
20	41	46.6	388	1	A37838
21	41	46.6	507	2	B96590
22	40	45.5	156	2	AD2745
23	40	45.5	156	2	C97526
24	40	45.5	249	2	A10704
25	40	45.5	254	2	A85410
26	40	45.5	439	2	B95149
27	40	45.5	439	2	D98017
28	40	45.5	458	2	E97349
29	40	45.5	580	2	C82082

30	40	45.5	645	2	E84042	threonyl-tRNA synth
31	40	45.5	1020	2	G88208	protein K02A2.3 (1
32	40	45.5	1448	2	A12007	Subtilase family p
33	39	44.3	100	2	AE0796	NADH2 dehydrogenas
34	39	44.3	100	2	B64999	NADH2 dehydrogenas
35	39	44.3	100	2	D85868	NADH2 dehydrogenase
36	39	44.3	100	2	C91024	NADH2 dehydrogenase
37	39	44.3	101	2	S37068	NADH2 dehydrogenase
38	39	44.3	126	2	J80331	SecE protein - Vib
39	39	44.3	140	2	S57063	probable membrane
40	39	44.3	162	2	C82765	conserved hypotet
41	39	44.3	176	2	AF3243	conjugal transfer
42	39	44.3	176	2	T03420	traF protein - Agr
43	39	44.3	220	2	H71360	probable thiamin A
44	39	44.3	220	2	AH3231	conjugal transfer
45	39	44.3	232	2	B69694	ribosomal protein

ALIGNMENTS

RESULT 1

A49528 Probable structural component p40 - Borna disease virus

N:Alternate names: 39K antigen

C:Species: borna disease virus

C:Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text change 28-Jul-2000

C:Accession: A49528; A37475; S25642; A44004

R:Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A:Title: Sequence conservation in field and experimental isolates of Borna disease vir

A:Reference number: A49528; MUID:94076462; PMID:8254777

A:Accession: A49528

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-370 <SCH>

A:Cross-references: UNIPARC:UPI000017106B; GB:S67502; NID:G456883; PIDN:AB29214.1; PI

A:Note: Sequence extracted from NCBI backbone (NCBIN:141399, NCBIPI:141401)

R:Pyper, U.M.; Richt, J.A.; Brown, L.; Kott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A:Title: Genomic organization of the structural proteins of borna disease virus reveal

A:Reference number: A37475; MUID:9303922; PMID:8317098

A:Accession: A37475

A:Molecule type: mRNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A:Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:G386390; PIDN:AB27261.1; PI

A:Note: Sequence extracted from NCBI backbone (NCBIN:134146, NCBIPI:134147)

A:Note: parts of this sequence were confirmed by peptide sequencing

R:Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Kott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A:Description: The 39/39K antigen of borna disease virus.

A:Reference number: S25642

A:Accession: S25642

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A:Cross-references: UNIPARC:UPI0000170E05; EMBL:X68392; NID:G58687; PIDN:CAA48458.1; P

A:Molecule type: genomic RNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <WCC>

A:Cross-references: UNIPARC:UPI0000170E06; GB:M99375; NID:G210698; PIDN:AAA73385.1; PI

C:Superfamily: borna disease virus p40

Query Match 90.9%; Score 80; DB 2; Length 370;
Best Local Similarity 88.9%; Pred. No. 3.6e-05;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

CM protein - protein search, using SW model

Run on: January 17, 2006, 15:55:45 / Search time 1.25241 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88

Sequence: 1 ELSGEISAIKRMIGTGLV 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database: Published Applications AA New*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/FC1_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	45.5	286	6	US-10-454-437-78
2	39	44.3	268	7	US-11-082-389-300
3	38	43.2	412	7	US-11-055-822-1086
4	38	43.2	533	6	US-10-467-657-2868
5	37	42.0	253	7	US-11-054-515-1859
6	37	42.0	322	6	US-10-524-647-18
7	37	42.0	565	6	US-10-793-626-2608
8	37	42.0	645	6	US-10-793-626-1770
9	36	40.9	564	6	US-10-517-939-288
10	35.5	40.3	197	7	US-11-082-389-114
11	35	39.8	240	7	US-11-082-389-166
12	35	39.8	259	6	US-10-454-437-292
13	35	39.8	266	7	US-11-055-822-620
14	35	39.8	408	7	US-11-082-389-164
15	35	39.8	760	7	US-11-052-534A-375
16	34.5	39.2	248	6	US-10-467-657-4404
17	34	38.6	48	7	US-11-011-666-8
18	34	38.6	73	6	US-10-485-517-229
19	34	38.6	122	6	US-10-821-234-1638
20	34	38.6	252	6	US-10-467-657-2206
21	34	38.6	254	6	US-11-054-515-1522
22	34	38.6	268	6	US-10-467-657-4064
23	34	38.6	275	7	US-11-065-943-54
24	34	38.6	287	6	US-10-793-626-1146
25	34	38.6	314	6	US-10-485-517-230

26	34	38.6	341	6	US-10-858-730-124	Sequence 124, App
27	34	38.6	376	7	US-11-082-389-122	Sequence 122, App
28	34	38.6	376	7	US-11-082-389-124	Sequence 124, App
29	34	38.6	533	6	US-10-467-657-8	Sequence 8, Appl
30	34	38.6	567	6	US-10-467-657-4328	Sequence 4328, Ap
31	34	38.6	729	7	US-11-210-316-29	Sequence 29, Appl
32	34	38.6	737	7	US-11-210-316-8	Sequence 29, Appl
33	34	38.6	744	7	US-11-052-554A-94	Sequence 94, Appl
34	33.5	38.1	226	6	US-10-878-556A-185	Sequence 185, App
35	33.5	38.1	463	6	US-10-531-844-2	Sequence 2, Appl
36	33	37.5	99	6	US-10-999-866-17	Sequence 17, Appl
37	33	37.5	99	7	US-11-084-554-200	Sequence 200, App
38	33	37.5	99	7	US-11-061-821-17	Sequence 17, Appl
39	33	37.5	109	7	US-11-064-174-61	Sequence 61, Appl
40	33	37.5	114	7	US-11-064-174-62	Sequence 62, Appl
41	33	37.5	119	6	US-10-485-788A-770	Sequence 770, Appl
42	33	37.5	119	7	US-11-053-076-147	Sequence 147, App
43	33	37.5	166	6	US-10-793-626-1576	Sequence 1576, Ap
44	33	37.5	236	6	US-10-793-626-998	Sequence 998, App
45	33	37.5	248	6	US-10-454-437-364	Sequence 364, App

ALIGNMENTS

RESULT 1
US-10-454-437-78
Sequence 78, Application US/10454437
GENERAL INFORMATION:
Publication No. US20050277115A1
APPLICANT: Pompeju, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Zeldner, Oskar
APPLICANT: Haberhauser, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
FILE REFERENCE: BGI-128CEN
CURRENT APPLICATION NUMBER: US/10/454,437
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 442
SEQ ID NO 78
LENGTH: 286
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-10-454-437-78
Query Match 45.5%; Score 40; DB 6; Length 286;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
CY 1 ELSGEISAIKRMIG 14

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 11.8215 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88

Sequence: 1.ELSGEISAIMRMIGVTGLV 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main:*

- 1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	4	US-10-627-141-41
2	46	52.3	89	4	US-10-109-048-574
3	46	52.3	89	4	US-10-109-048-575
4	46	52.3	89	4	US-10-109-048-577
5	46	52.3	89	4	US-10-109-048-781
6	46	52.3	89	4	US-10-109-048-782
7	46	52.3	119	4	US-10-109-048-121
8	46	52.3	119	4	US-10-109-048-122
9	46	52.3	119	4	US-10-109-048-123
10	46	52.3	119	4	US-10-109-048-124
11	46	52.3	119	4	US-10-109-048-125
12	46	52.3	119	4	US-10-109-048-126
13	46	52.3	119	4	US-10-109-048-127
14	46	52.3	119	4	US-10-109-048-128
15	46	52.3	119	4	US-10-109-048-129
16	46	52.3	119	4	US-10-109-048-130
17	46	52.3	119	4	US-10-109-048-131
18	46	52.3	119	4	US-10-109-048-132
19	46	52.3	119	4	US-10-109-048-133
20	46	52.3	119	4	US-10-109-048-134
21	46	52.3	119	4	US-10-109-048-135
22	46	52.3	119	4	US-10-109-048-136
23	46	52.3	119	4	US-10-109-048-137
24	46	52.3	119	4	US-10-109-048-138
25	46	52.3	119	4	US-10-109-048-139
26	46	52.3	119	4	US-10-109-048-140
27	46	52.3	119	4	US-10-109-048-142

28	46	52.3	119	4	US-10-109-048-143	Sequence 143, App
29	46	52.3	119	4	US-10-109-048-144	Sequence 144, App
30	46	52.3	119	4	US-10-109-048-145	Sequence 145, App
31	46	52.3	185	4	US-10-109-048-434	Sequence 435, App
32	46	52.3	185	4	US-10-109-048-435	Sequence 436, App
33	46	52.3	185	4	US-10-109-048-436	Sequence 437, App
34	46	52.3	185	4	US-10-109-048-437	Sequence 438, App
35	46	52.3	468	4	US-10-425-114-41880	Sequence 41880, A
36	46	52.3	468	4	US-10-425-114-51072	Sequence 51072, A
37	46	52.3	472	4	US-10-425-114-36908	Sequence 36908, A
38	46	52.3	533	4	US-10-628-525-5	Sequence 5, App1
39	46	52.3	591	4	US-10-425-115-339970	Sequence 339970, A
40	46	52.3	600	4	US-10-272-291-3	Sequence 3, App1
41	46	52.3	600	4	US-10-272-291-4	Sequence 4, App1
42	46	52.3	604	6	US-11-004-536-4	Sequence 6, App1
43	46	52.3	604	6	US-11-004-536-6	Sequence 6, App1
44	46	52.3	605	4	US-10-272-291-6	Sequence 6, App1
45	46	52.3	605	4	US-10-109-048-34	Sequence 34, App1

ALIGNMENTS

RESULT 1
US-10-627-141-41
Sequence 41, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-627-141-41
Query Match 100.0%; Score 88; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 3.29904 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-41

Sequence: 1 ELSGEISAIWMIGVTGLV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RB.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	2	US-08-779-764A-41
2	88	100.0	19	2	US-09-563-456-41
3	81	92.0	370	12	US-08-369-822C-2
4	81	92.0	370	2	US-08-582-776C-2
5	81	92.0	370	2	US-08-434-831B-2
6	47	53.4	300	2	US-09-489-039A-9673
7	46	52.3	533	2	US-08-941-445A-5
8	46	52.3	604	2	US-09-731-166-4
9	46	52.3	609	2	US-08-941-445A-7
10	45	51.1	820	2	US-09-902-540-16384
11	44	50.0	420	2	US-09-066-047-8
12	43	48.9	89	2	US-09-328-352-5209
13	43	48.9	90	1	US-08-341-219-24
14	43	48.9	90	2	US-08-912-314A-24
15	43	48.9	116	2	US-09-543-681A-6674
16	41.5	47.2	495	2	US-08-984-618-5
17	40	45.5	100	2	US-09-634-955B-29
18	40	45.5	166	2	US-09-583-110-4509
19	40	45.5	168	2	US-08-858-207A-486
20	40	45.5	207	2	US-09-634-955B-28
21	40	45.5	266	2	US-09-602-772A-78
22	40	45.5	365	2	US-09-328-352-7147
23	40	45.5	415	2	US-09-540-236-2213
24	40	45.5	444	2	US-09-861-451A-16
25	39	44.3	59	2	US-09-902-540-13434
26	39	44.3	99	2	US-09-248-796A-18575
27	39	44.3	140	1	US-08-691-071-4

28	39	44.3	140	1	US-08-843-370-4	Sequence 4, Appli
29	39	44.3	157	2	US-10-104-047-3538	Sequence 3538, Ap
30	39	44.3	159	2	US-09-489-039A-12575	Sequence 12575, A
31	39	44.3	308	2	US-09-252-991A-18081	Sequence 18081, A
32	39	44.3	322	2	US-09-107-532A-5708	Sequence 5708, Ap
33	39	44.3	359	1	US-08-976-074-5	Sequence 5, Appli
34	39	44.3	359	1	US-08-083-741-5	Sequence 5, Appli
35	39	44.3	359	2	US-08-976-166A-5	Sequence 5, Appli
36	39	44.3	366	2	US-09-058-725B-4	Sequence 4, Appli
37	39	44.3	386	2	US-09-232-857-4	Sequence 4, Appli
38	39	44.3	409	2	US-09-068-804-42	Sequence 42, Appli
39	39	44.3	410	2	US-09-068-804-6	Sequence 6, Appli
40	39	44.3	512	1	US-08-173-508-4	Sequence 4, Appli
41	39	44.3	512	1	US-08-265-310-4	Sequence 4, Appli
42	39	44.3	512	2	US-08-951-742-4	Sequence 4, Appli
43	39	44.3	733	2	US-09-328-352-5599	Sequence 5599, Ap
44	39	43.2	53	2	US-09-621-976-7442	Sequence 7442, Ap
45	38	43.2	53	2	US-09-621-976-7444	Sequence 7444, Ap

ALIGNMENTS

RESULT 1
US-08-779-764A-41
Sequence 41, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPTS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-779-764A-41

Query Match 100.0% ; Score 88; DB 2; Length 19;
Best Match Similarity 100.0% ; Pred. No. 1.3e+08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELSGEISAIWMIGVTGLV 19
|||||
Db 1 ELSGEISAIWMIGVTGLV 19

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 17, 2006, 15:30:13 ; Search time 11.3939 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-41
Perfect score: 88
Sequence: 1 ELSGEISAIMRMIGVTGLV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	95.5	370	1 VP40 BDV	Q01552 borna disease
2	84	95.5	370	2 0774B9 BDV	Q07469 borna disease
3	81	92.0	369	2 0909V1 BDV	Q09091 borna disease
4	81	92.0	370	2 010392 BDV	Q010392 borna disease
5	81	92.0	370	2 010395 BDV	Q010395 borna disease
6	81	92.0	370	2 010401 BDV	Q010401 borna disease
7	81	92.0	370	2 05GL50 BDV	Q05GL50 borna disease
8	81	92.0	370	2 05GL62 BDV	Q05GL62 borna disease
9	81	92.0	370	2 05GL71 BDV	Q05GL71 borna disease
10	81	92.0	370	2 05GL92 BDV	Q05GL92 borna disease
11	81	92.0	370	2 05GL95 BDV	Q05GL95 borna disease
12	81	92.0	370	2 05GL98 BDV	Q05GL98 borna disease
13	81	92.0	370	2 05GLB3 BDV	Q05GLB3 borna disease
14	81	92.0	370	2 05GLC8 BDV	Q05GLC8 borna disease
15	81	92.0	370	2 08B829 BDV	Q08B829 borna disease
16	81	92.0	370	2 0910H1 BDV	Q0910H1 borna disease
17	81	92.0	370	2 091UL4 BDV	Q091UL4 borna disease
18	81	92.0	370	2 091UL8 BDV	Q091UL8 borna disease
19	80	90.9	370	2 010398 BDV	Q010398 borna disease
20	80	90.9	370	2 05GL186 BDV	Q05GL186 borna disease
21	80	90.9	370	2 05GL187 BDV	Q05GL187 borna disease
22	48	54.5	123	2 08TMI8 METAC	Q08TMI8 methanobarc
23	48	54.5	256	2 09AME8 PYKAO	Q09AME8 elymus glau
24	48	54.5	358	2 05UDP0 PYKAO	Q05UDP0 pyrococcus
25	47	53.4	188	2 08ZYR2 PYRAB	Q08ZYR2 pyrobaulium
26	47	53.4	254	2 081590 ANOMA	Q081590 anomochloa
27	47	53.4	255	2 081558 GPOLAL	Q081558 schizachyri
28	47	53.4	373	2 07N116 GLOVI	Q07N116 gloebacter
29	47	53.4	537	2 0522N2 MAGGR	Q0522N2 magnaporthe
30	46	52.3	90	2 0513B4 MORAL	Q0513B4 monopterus
31	46	52.3	244	2 081539 GPOLAL	Q081539 arundinella

32	46	52.3	246	2	081560 ZEAU	Q081560 zea luxuria
33	46	52.3	247	2	081596 MELCU	Q081596 melica cupa
34	46	52.3	248	2	06UTV5 GPOLAL	Q06UTV5 elymus repe
35	46	52.3	249	2	06UTV2 TAECM	Q06UTV2 taeniathecu
36	46	52.3	249	2	06UTV7 GPOLAL	Q06UTV7 elymus repe
37	46	52.3	249	2	06UTV8 GPOLAL	Q06UTV8 elymus repe
38	46	52.3	249	2	06UTV1 GPOLAL	Q06UTV1 elymus repe
39	46	52.3	249	2	06UTV2 GPOLAL	Q06UTV2 elymus repe
40	46	52.3	249	2	06UTV4 GPOLAL	Q06UTV4 elymus repe
41	46	52.3	249	2	06UTV5 GPOLAL	Q06UTV5 elymus repe
42	46	52.3	249	2	06UTV6 GPOLAL	Q06UTV6 elymus repe
43	46	52.3	249	2	06UTV8 GPOLAL	Q06UTV8 elymus repe
44	46	52.3	249	2	06UTV0 GPOLAL	Q06UTV0 elymus repe
45	46	52.3	249	2	06UTV4 GPOLAL	Q06UTV4 elymus repe

ALIGNMENTS

RESULT 1	ID	VP40 BDV	STANDARD	PRT	370 AA.
AC	Q01552				
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	13-SEP-2005	(Rel. 48, Last annotation update)			
DE	40 kDa protein.				
CN	Name=PA0; Synonyms=P38;				
OS	Borna disease virus (BDV).				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;				
OC	Bornavirinae.				
OX	NCBI_TaxID=12455;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=C6;				
RX	MEDLINE=94149825; PubMed=8317098;				
RA	Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.B.;				
RT	Cubitt B., Oldstone C., de la Torre J.C.;				
RT	"Sequence and genome organization of Borna disease virus.";				
RL	J. Virol. 68:1382-1396(1994).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.				
RC	STRAIN=Clone B8;				
RX	MEDLINE=93303922; PubMed=8317098;				
RA	Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.B.;				
RT	"Genomic organization of the structural proteins of Borna disease virus revealed by a cDNA clone encoding the 38-kDa protein.";				
RL	Virology 195:229-238(1993).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE OF 10-370.				
RC	STRAIN=Giessen / HR/80-3;				
RA	Birz T., Riehle H., Yamasaki J., Richt J.A., Grebenstein O., Rott R.,				
RT	Niemann H.;				
RT	Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Halle BI/91;				
RX	MEDLINE=94076462; PubMed=8254777;				
RA	Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;				
RT	"Sequence conservation in field and experimental isolates of Borna disease virus.";				
RL	J. Virol. 68:63-68(1994).				
RN	[5]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=V;				
RX	MEDLINE=94240137; PubMed=8183914;				
RA	Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H.,				
RT	Lipkin W.I.;				
RT	"Genomic organization of Borna disease virus.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).				
RN	[6]				
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.				
RC	STRAIN=HR/80-1;				
RX	MEDLINE=93021385; PubMed=1404604;				

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 1.1865 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-40

Sequence: 1 MEDQDLYEPASLPKLP 18

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	42.9	1075	6	US-10-821-234-1202	Sequence 1202, App
2	40	40.8	282	6	US-10-972-587-28	Sequence 28, Appl
3	40	40.8	412	6	US-10-524-919-2	Sequence 2, Appl
4	40	40.8	1024	6	US-10-131-826A-198	Sequence 198, Appl
5	39	39.8	798	7	US-11-110-082-39	Sequence 39, Appl
6	38	38.8	358	7	US-11-055-822-572	Sequence 572, App
7	38	38.8	358	7	US-11-055-822-836	Sequence 836, App
8	38	38.8	477	7	US-11-055-822-98	Sequence 98, Appl
9	38	38.8	477	7	US-11-186-284-127	Sequence 127, Appl
10	38	38.8	535	6	US-10-793-626-1024	Sequence 1024, App
11	37.5	38.3	406	7	US-11-107-028-7	Sequence 7, Appl
12	37	37.8	132	6	US-10-821-234-1249	Sequence 1249, App
13	37	37.8	151	6	US-10-131-826A-508	Sequence 508, App
14	37	37.8	179	6	US-10-467-657-5942	Sequence 5942, App
15	37	37.8	267	7	US-11-056-408-4	Sequence 4, Appl
16	37	37.8	284	7	US-11-056-408-10	Sequence 10, Appl
17	37	37.8	347	6	US-10-821-234-1379	Sequence 1379, App
18	37	37.8	437	6	US-10-453-372-438	Sequence 438, App
19	37	37.8	633	7	US-11-063-343-26	Sequence 26, Appl
20	37	37.8	676	6	US-10-453-372-440	Sequence 440, Appl
21	37	37.8	730	6	US-10-453-372-444	Sequence 444, Appl
22	37	37.8	737	6	US-10-453-372-434	Sequence 434, Appl
23	37	37.8	737	6	US-10-453-372-446	Sequence 446, Appl
24	37	37.8	737	6	US-10-453-372-448	Sequence 448, Appl
25	37	37.8	737	6	US-10-453-372-450	Sequence 450, Appl

26	37	37.8	737	6	US-10-453-372-452	Sequence 452, App
27	37	37.8	737	6	US-10-453-372-454	Sequence 454, App
28	37	37.8	737	6	US-10-453-372-456	Sequence 456, App
29	37	37.8	737	6	US-11-052-554A-141	Sequence 141, App
30	36	36.7	111	6	US-10-845-413-69	Sequence 69, Appl
31	36	36.7	111	6	US-10-845-413-70	Sequence 70, Appl
32	36	36.7	310	7	US-11-074-176-108	Sequence 108, App
33	36	36.7	312	6	US-10-986-501-124	Sequence 124, App
34	36	36.7	338	6	US-10-517-939-82	Sequence 82, Appl
35	36	36.7	411	6	US-10-524-919-4	Sequence 4, Appl
36	36	36.7	545	7	US-11-134-563-16	Sequence 16, Appl
37	36	36.7	888	6	US-10-131-826A-544	Sequence 544, App
38	36	36.7	1330	6	US-10-453-372-260	Sequence 260, App
39	36	36.7	1542	6	US-10-453-372-258	Sequence 258, App
40	36	36.7	1542	6	US-10-453-372-266	Sequence 266, App
41	36	36.7	1542	6	US-10-453-372-280	Sequence 280, App
42	35	35.7	128	6	US-10-467-657-2492	Sequence 2492, App
43	35	35.7	129	6	US-10-467-657-2496	Sequence 2496, App
44	35	35.7	143	7	US-11-102-883-12	Sequence 12, Appl
45	35	35.7	263	7	US-11-102-883-36	Sequence 36, Appl

ALIGNMENTS

```

RESULT 1
US-10-821-234-1202
; Sequence 1202, Application US/10821234
; Publication No. US200502551141
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc seq_genes Version 1.0
; SEQ ID NO 1202
; LENGTH: 1075
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1202

Query Match      42.9%; Score 42; DB 6; Length 1075;
Best Local Similarity 53.8%; Pred. NO. 55;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Cy      4 QDDLYEPASLPK 16
Db      391 EDDYSPSKRPK 403

RESULT 2
US-10-972-587-28
; Sequence 28, Application US/10972587
; Publication No. US20050246799A1
; GENERAL INFORMATION:
; APPLICANT: Song, Xiaoling
; APPLICANT: Bartola, Pauline Anne
; APPLICANT: Linderoth, Nora Abiella
; APPLICANT: Fan, Hao
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICITORS AND
; FILE REFERENCE: 21829/213
; CURRENT APPLICATION NUMBER: US/10/972.587
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: 60/335,776

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 11.1994 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-40

Sequence: 1 MEDODLYEPAPLKP 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	US-10-627-141-40	Sequence 40, Appl
2	50	51.0	536	US-11-097-143-7113	Sequence 7113, Ap
3	49	50.0	116	US-10-767-701-50219	Sequence 50219, A
4	49	50.0	630	US-10-259-194A-40	Sequence 40, Appl
5	48	49.0	68	US-10-424-599-215266	Sequence 215266,
6	48	49.0	415	US-10-425-114-48445	Sequence 48445, A
7	48	49.0	456	US-10-437-963-16587	Sequence 16587,
8	47	48.0	68	US-10-681-207-5	Sequence 5, Appl1
9	47	48.0	141	US-10-424-599-151574	Sequence 151574,
10	47	48.0	236	US-10-767-701-40843	Sequence 40843, A
11	47	48.0	623	US-11-097-143-40044	Sequence 40044, A
12	46.5	47.4	357	US-10-282-122A-76274	Sequence 76274, A
13	46	46.9	349	US-10-437-963-162980	Sequence 162980,
14	46	46.9	541	US-10-128-714-8184	Sequence 8184, Ap
15	46	46.9	1369	US-11-097-143-8309	Sequence 9309, Ap
16	46	46.9	6239	US-10-156-761-8477	Sequence 8477, Ap
17	46	46.9	6239	US-10-204-862A-5	Sequence 4, Appl1
18	46	46.9	6239	US-11-005-196-4	Sequence 4, Appl1
19	45	45.9	429	US-10-437-963-126338	Sequence 126338,
20	45	45.9	474	US-11-097-143-26433	Sequence 26433, A
21	45	45.9	488	US-10-282-122A-51581	Sequence 51581, A
22	45	45.9	700	US-10-282-122A-51105	Sequence 51105, A
23	44	44.9	74	US-11-111-953-725	Sequence 725, App
24	44	44.9	105	US-10-424-599-148059	Sequence 148059,
25	44	44.9	193	US-10-767-701-61319	Sequence 61319, A
26	44	44.9	292	US-10-437-963-180963	Sequence 180963,
27	44	44.9	396	US-10-424-599-218884	Sequence 218884,

28	44	44.9	441	US-10-437-963-173638	Sequence 173638,
29	44	44.9	593	US-10-437-963-133881	Sequence 133881,
30	44	44.9	619	US-10-732-923-19401	Sequence 19401, A
31	44	44.9	656	US-10-032-585-7598	Sequence 7598, Ap
32	44	44.9	1028	US-10-369-493-3464	Sequence 3464, Ap
33	44	44.9	3536	US-11-097-143-23232	Sequence 23232, A
34	43.5	44.4	520	US-09-976-782-26	Sequence 26, Appl
35	43	43.9	93	US-10-425-115-278438	Sequence 278438,
36	43	43.9	107	US-10-424-599-215820	Sequence 215820,
37	43	43.9	122	US-10-094-749-2208	Sequence 2208, Ap
38	43	43.9	142	US-10-425-115-214635	Sequence 214635,
39	43	43.9	146	US-10-767-701-32214	Sequence 32214, A
40	43	43.9	150	US-10-424-599-273725	Sequence 273725,
41	43	43.9	189	US-10-425-115-338098	Sequence 338098,
42	43	43.9	203	US-10-282-122A-66541	Sequence 66541, A
43	43	43.9	219	US-10-108-260A-3657	Sequence 3657, Ap
44	43	43.9	222	US-10-739-930-9785	Sequence 9785, Ap
45	43	43.9	258	US-10-408-765A-878	Sequence 878, App

ALIGNMENTS

RESULT 1
US-10-627-141-40
; Sequence 40, Application US/10627141
; Publication No. US20040162421A1
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,141
; FILING DATE: 25-Jul-2003
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-627-141-40
Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDODLYEPAPLKP 18

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 3.1254 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDIYEPASLPKLP 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PTCUB.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	2	US-08-779-764A-40 Sequence 40, Appl
2	98	100.0	18	2	US-09-563-456-40 Sequence 40, Appl
3	81.5	83.2	370	2	US-08-369-822C-2 Sequence 2, Appl
4	81.5	83.2	370	2	US-08-582-776C-2 Sequence 2, Appl
5	81.5	83.2	370	2	US-08-434-831B-2 Sequence 2, Appl
6	50	51.0	451	2	US-09-248-796A-15169 Sequence 15169, A
7	47	48.0	66	2	US-08-945-998A-2 Sequence 2, Appl
8	46	46.9	153	2	US-09-270-767-33096 Sequence 33096, A
9	46	46.9	153	2	US-09-270-767-48313 Sequence 48313, A
10	46	46.9	6239	2	US-09-914-286-4 Sequence 4, Appl
11	44	44.9	501	2	US-09-538-092-707 Sequence 707, App
12	44	44.9	660	2	US-09-248-796A-14578 Sequence 14578, A
13	43.5	44.4	465	2	US-09-252-991A-20576 Sequence 20576, A
14	43	43.4	320	2	US-09-252-991A-18243 Sequence 18243, A
15	42.5	43.9	25	1	US-08-942-423-26 Sequence 26, Appl
16	42	42.9	72	2	US-09-248-796A-24571 Sequence 24571, A
17	42	42.9	744	2	US-09-248-796A-17662 Sequence 17662, A
18	42	42.9	806	2	US-09-248-796A-15961 Sequence 15961, A
19	42	42.9	2183	2	US-08-746-111-5 Sequence 5, Appl
20	41	41.8	32	2	US-09-314-268-122 Sequence 122, App
21	41	41.8	47	1	US-08-659-251-37 Sequence 37, Appl
22	41	41.8	47	2	US-09-256-490-37 Sequence 37, Appl
23	41	41.8	47	4	PCT-US96-11445-37 Sequence 37, Appl
24	41	41.8	99	2	US-09-732-210-1583 Sequence 1583, Ap
25	41	41.8	148	2	US-09-248-796A-19533 Sequence 19533, A
26	41	41.8	204	2	US-09-540-236-3610 Sequence 3610, Ap
27	41	41.8	311	2	US-09-270-767-33374 Sequence 33374, A

28	41	41.8	311	2	US-09-270-767-48591 Sequence 48591, A
29	41	41.8	348	2	US-09-248-528-7 Sequence 7, Appl
30	41	41.8	348	2	US-09-549-108-7 Sequence 7, Appl
31	41	41.8	348	2	US-09-549-111-7 Sequence 7, Appl
32	41	41.8	348	2	US-09-549-106-7 Sequence 7, Appl
33	41	41.8	348	2	US-09-550-394-7 Sequence 14234, A
34	41	41.8	348	2	US-09-902-540-14234 Sequence 105, App
35	41	41.8	434	2	US-09-716-964B-105 Sequence 105, App
36	41	41.8	446	2	US-09-716-964B-100 Sequence 100, App
37	41	41.8	449	2	US-09-355-214-3 Sequence 3, Appl
38	41	41.8	456	1	US-08-819-013-1 Sequence 1, Appl
39	41	41.8	456	2	US-09-355-214-1 Sequence 1, Appl
40	41	41.8	470	2	US-09-949-016-7976 Sequence 7976, Ap
41	41	41.8	518	2	US-09-902-540-11108 Sequence 11108, A
42	41	41.8	546	2	US-09-252-991A-17104 Sequence 17104, A
43	41	41.8	586	2	US-09-252-991A-29920 Sequence 29920, A
44	41	41.8	2142	2	US-09-538-092-1142 Sequence 1142, Ap
45	41	41.8	2142	2	US-09-949-002-371 Sequence 371, App

ALIGNMENTS

RESULT 1
US-08-779-764A-40
Sequence 40, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pine Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-779-764A-40

Query Match 100.0%; Score 98; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MEDDDIYEPASLPKLP 18
DB 1 MEDDDIYEPASLPKLP 18

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 : Search time 10.7942 Seconds

(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDLYEPASLPKLP 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 216643 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 216643

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	83.2	370	1 VP40_BDV	001552 borna disea
2	81.5	83.2	370	2 O10392_BDV	010392 borna disea
3	81.5	83.2	370	2 O10395_BDV	010395 borna disea
4	81.5	83.2	370	2 O10398_BDV	010398 borna disea
5	81.5	83.2	370	2 O10401_BDV	010401 borna disea
6	81.5	83.2	370	2 O5GL50_BDV	05GL50 borna disea
7	81.5	83.2	370	2 O5GL71_BDV	05GL71 borna disea
8	81.5	83.2	370	2 O5GL86_BDV	05GL86 borna disea
9	81.5	83.2	370	2 O5GL92_BDV	05GL92 borna disea
10	81.5	83.2	370	2 O5GL98_BDV	05GL98 borna disea
11	81.5	83.2	370	2 O5GLB3_BDV	05GLB3 borna disea
12	81.5	83.2	370	2 O5GLB2_BDV	05GLB2 borna disea
13	81.5	83.2	370	2 O910H1_BDV	0910H1 borna disea
14	81.5	83.2	370	2 O910H4_BDV	0910H4 borna disea
15	81.5	83.2	370	2 O774B9_BDV	0774B9 borna disea
16	81.5	83.2	370	2 O5GL62_BDV	05GL62 borna disea
17	77.5	79.1	370	2 O5GL95_BDV	05GL95 borna disea
18	74.5	76.0	370	2 O5GLC8_BDV	05GLC8 borna disea
19	74.5	76.0	370	2 O5GLD1_BDV	05GLD1 borna disea
20	74.5	76.0	370	2 O909V1_BDV	0909V1 borna disea
21	72.5	74.0	369	2 O9M3B9_ARATH	09M3B9 arabidopsi
22	54	55.1	1408	2 O4RNY5_TETNG	04RNY5 tetradon n
23	53	54.1	490	2 O4WJL3_ASPFU	04WJL3 aspergillu
24	53	54.1	722	2 O4WJL3_ASPFU	04WJL3 aspergillu
25	52	53.1	370	2 O623X5_CAEBR	0623X5 caenorhabd
26	52	53.1	1299	2 O510B6_MAGGR	0510B6 magnaporth
27	51	52.0	201	2 O8LGR5_VITVI	08LGR5 vitis vinif
28	50	51.0	193	2 O95TB4_DROSOPHILA	095TB4 drosophila
29	50	51.0	311	2 O5AF05_CANAL	05AF05 candida alb
30	50	51.0	427	2 O9W0Z3_DROSOPHILA	09W0Z3 drosophila
31	50	51.0	536	2 O9W0Z3_DROSOPHILA	09W0Z3 drosophila

32	50	51.0	850	2 O9W0Z5_DROME	O9W0Z5 drosophila
33	50	51.0	913	2 O5U2Y1_RAT	O5U2Y1 rattus norv
34	49	50.0	309	2 O7GT59_GIALA	O7GT59 giardia lam
35	49	50.0	525	2 O7F0H9_ORISA	O7F0H9 oryza sativ
36	49	50.0	876	2 O60RM3_CAEBR	O60RM3 caenorhabd
37	48.5	49.5	389	2 O5G6S2_RCHIR	O5G6S2 rhyrchomyct
38	48.5	49.5	1055	2 O4RK41_TETNG	O4RK41 tetradon n
39	48	49.0	304	2 O5BKX8_HUMAN	O5BKX8 homo sapien
40	48	49.0	465	2 O523R8_MAGGR	O523R8 magnaporth
41	48	49.0	473	2 O6BPV7_DEBHA	O6BPV7 debaryomyce
42	48	49.0	764	2 O7SFS1_NEUCR	O7SFS1 neurospora
43	48	49.0	858	2 O7SEK3_ASHGO	O7SEK3 ashbya goss
44	47.5	48.5	527	2 O5R3Y6_CAEBL	O5R3Y6 caenorhabd
45	47.5	48.5	561	2 O95Q64_CAEBL	O95Q64 caenorhabd

ALIGNMENTS

RESULT 1	VP40_BDV	STANDARD;	PRT;	370 AA.
AC	O01552;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	40 kDa protein.			
GN	Name=P40; Synonyms=P38;			
OS	Borna disease virus (BDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;			
OC	Bornavirus.			
OX	NCBI_Taxid=12455;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=C6;			
RX	MEDLINE=94149825; PubMed=7906311;			
RT	"Genomic organization of the structural proteins of Borna disease virus revealed by a cDNA clone encoding the 38-kDa protein.";			
RT	Quiblit B., Oldstone C., de la Torre J.C.;			
RL	J. Virol. 68:1382-1396(1994).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.			
RC	STRAIN=Clone B8;			
RX	MEDLINE=93303922; PubMed=8317098;			
RT	Pyper J.W., Richt J.A., Brown L., Rott R., Narayan O., Clements J.E.;			
RT	"Genomic organization of the structural proteins of Borna disease virus revealed by a cDNA clone encoding the 38-kDa protein.";			
RL	Virol. 195:229-238(1993).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE OF 10-370.			
RC	STRAIN=Giesse / HE/80-3;			
RA	Binz T., Riehle H., Yamasaki J., Richt J.A., Grebenstein O., Rott R.,			
RA	Niemann H.;			
RT	Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Halle B1/91;			
RX	MEDLINE=9407462; PubMed=8254777;			
RT	Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;			
RT	"Sequence conservation in field and experimental isolates of Borna disease virus.";			
RL	J. Virol. 68:63-68(1994).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=V;			
RX	MEDLINE=94240137; PubMed=8183914;			
RA	Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H.,			
RA	Lipkin W.I.;			
RT	"Genomic organization of Borna disease virus.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.			
RC	STRAIN=HE/80-1;			
RX	MEDLINE=93021385; PubMed=1404604;			

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 1.73633 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDLYEPKSLPKLP 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	83.2	370	2	A49528
2	54	53.1	1408	2	T47671
3	52	53.1	370	2	AB2490
4	47.5	48.5	721	2	D87753
5	47	48.0	309	2	G87498
6	47	48.0	1743	2	T15893
7	46.5	47.4	357	2	AD1062
8	46	46.9	1545	2	T26589
9	45	45.9	488	2	P97066
10	45	45.9	1217	2	T22672
11	44	44.9	366	2	B84265
12	44	44.9	501	2	B66763
13	44	44.9	533	2	B56110
14	44	44.9	784	2	AP1638
15	43	43.9	116	2	A72641
16	43	43.9	203	2	B83176
17	43	43.9	279	2	H90966
18	43	43.9	279	2	C85832
19	43	43.9	279	2	B64972
20	43	43.9	283	2	G88349
21	43	43.9	283	2	T27027
22	43	43.9	392	1	FOLJGA
23	43	43.9	392	1	FOLJGB
24	43	43.9	393	2	S29356
25	43	43.9	495	2	T00811
26	43	43.9	505	2	T37975
27	43	43.9	510	2	H69893
28	43	43.9	625	2	T16777
29	43	43.9	670	2	T37483

30	43	43.9	903	2	T00358	hypothetical prote
31	43	43.9	1298	2	T47523	DNA-binding protei
32	42.5	43.4	738	2	T27289	hypothetical prote
33	42.5	43.4	1711	2	T11432	hypothetical prote
34	42	42.9	208	2	S00449	photosystem I chal
35	42	42.9	286	2	F87075	membrane transport
36	42	42.9	317	2	S72851	hypothetical prote
37	42	42.9	501	2	T16084	hypothetical prote
38	42	42.9	569	2	B84904	probable lactase (
39	42	42.9	623	2	S56206	probable membrane
40	42	42.9	775	2	B64319	carbon-monoxide de
41	42	42.9	957	2	T03829	transcription fact
42	42	42.9	998	2	T09492	general transcript
43	42	42.9	2183	2	T42764	coagulation factor
44	41.5	42.3	992	2	S49835	hypothetical prote
45	41.5	42.3	1225	2	T16346	hypothetical prote

ALIGNMENTS

RESULT 1

probable structural component p40 - Borna disease virus

N:Alternate names: 39K antigen

C:Species: borna disease virus

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000

C:Accession: A49528; A37475; S25642; A44004

R:Schneider, P.A.; Briese, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A>Title: Sequence conservation in field and experimental isolates of Borna disease vir

A:Reference number: A49528; MUID:94076462; PMID:8254777

A:Accession: A49528

A>Status: Preliminary

A:Molecule type: genomic RNA

A:Residues: 1-370 <SCH>

A:Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:9386390; PIDN:AA829214.1; PI

A:Note: sequence extracted from NCBI backbone (NCBI:134145, NCBI:P.141401)

A:Experimental source: WT-1, Halle B1/91, horse brain, field isolate

R:Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A>Title: Genomic organization of the structural proteins of Borna disease virus reveal

A:Reference number: A37475; MUID:93303922; PMID:8317098

A:Accession: A37475

A:Molecule type: mRNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <DYP>

A:Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:9386390; PIDN:AA829214.1; PI

A:Note: sequence extracted from NCBI backbone (NCBI:134145, NCBI:P.134147)

A:Note: parts of this sequence were confirmed by peptide sequencing

R:Binz, T.; Richt, H.; Yamaoka, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A:Description: The 39/39K antigen of Borna disease virus.

A:Reference number: S25642

A:Accession: S25642

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A:Cross-references: UNIPARC:UPI0000170E05; EMBL:X68392; NID:958687; PIDN:CAA48458.1; P

R:McClure, M.A.; Thibault, K.J.; Hataleki, C.G.; Lipkin, W.I.

J. Virol. 66, 6572-6577, 1992

A>Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w

A:Reference number: A44004; MUID:93021385; PMID:11404604

A:Accession: A44004

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 14-46, 'I', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A:Cross-references: UNIPARC:UPI0000170E06; GB:M9375; NID:9210698; PIDN:AA73385.1; PI

C:Superfamily: borna disease virus p40

Query Match 83.2%; Score 81.5; DB 2; Length 370;
Best Local Similarity 94.4%; Pred. No. 4.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 17, 2006, 15:28:28 ; Search time 11.9228 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDLYEPPASLPKLP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	98	100.0	18	2	AAW49062 Human Bor
2	81.5	83.2	370	2	AAW49062 Human Bor
3	54	55.1	1351	3	AAW49062 Human Bor
4	50	51.0	20	7	AAW49062 Human Bor
5	50	51.0	536	4	AAW49062 Human Bor
6	48	49.0	364	8	AAW49062 Human Bor
7	48	49.0	415	8	AAW49062 Human Bor
8	48	49.0	415	8	AAW49062 Human Bor
9	47	48.0	20	7	AAW49062 Human Bor
10	47	48.0	20	7	AAW49062 Human Bor
11	47	48.0	20	7	AAW49062 Human Bor
12	47	48.0	20	7	AAW49062 Human Bor
13	47	48.0	66	2	AAW49062 Human Bor
14	47	48.0	66	2	AAW49062 Human Bor
15	47	48.0	66	2	AAW49062 Human Bor
16	47	48.0	161	7	AAW49062 Human Bor
17	47	48.0	161	7	AAW49062 Human Bor
18	47	48.0	161	7	AAW49062 Human Bor
19	47	48.0	623	4	AAW49062 Human Bor
20	46.5	47.4	357	6	AAW49062 Human Bor
21	46	46.9	14	7	AAW49062 Human Bor
22	46	46.9	16	7	AAW49062 Human Bor
23	46	46.9	17	7	AAW49062 Human Bor
24	46	46.9	18	7	AAW49062 Human Bor

25	46	46.9	18	7	AAW49062 Human Bor
26	46	46.9	19	7	AAW49062 Human Bor
27	46	46.9	19	7	AAW49062 Human Bor
28	46	46.9	20	7	AAW49062 Human Bor
29	46	46.9	20	7	AAW49062 Human Bor
30	46	46.9	20	7	AAW49062 Human Bor
31	46	46.9	20	7	AAW49062 Human Bor
32	46	46.9	20	7	AAW49062 Human Bor
33	46	46.9	20	7	AAW49062 Human Bor
34	46	46.9	20	7	AAW49062 Human Bor
35	46	46.9	20	7	AAW49062 Human Bor
36	46	46.9	541	6	AAW49062 Human Bor
37	46	46.9	1369	4	AAW49062 Human Bor
38	46	46.9	6239	3	AAW49062 Human Bor
39	46	46.9	6239	3	AAW49062 Human Bor
40	45	45.9	20	7	AAW49062 Human Bor
41	45	45.9	20	7	AAW49062 Human Bor
42	45	45.9	20	7	AAW49062 Human Bor
43	45	45.9	488	6	AAW49062 Human Bor
44	45	45.9	490	9	AAW49062 Human Bor
45	45	45.9	644	3	AAW49062 Human Bor

ALIGNMENTS

RESULT 1	AAW49062	standard; peptide; 18 AA.
XX	AAW49062;	
AC	AAW49062;	
XX	AAW49062;	
DT	27-AUG-2003 (revised)	
DT	09-NOV-1998 (first entry)	
XX	Human Borna disease virus p40 peptide.	
DE	Human Borna disease virus p40 peptide.	
XX	BDV; infection; diagnosis; neuropsychiatric disorder; human.	
KW	BDV; infection; diagnosis; neuropsychiatric disorder; human.	
OS	Borna disease virus.	
XX	W09830238-A1.	
PN	W09830238-A1.	
XX	16-JUL-1998.	
PD	16-JUL-1998.	
XX	07-JAN-1998; 98WO-US000495.	
PF	07-JAN-1998; 98WO-US000495.	
XX	07-JAN-1997; 97US-00779764.	
PR	07-JAN-1997; 97US-00779764.	
XX	(SCRI) SCRIIPS RES INST.	
PA	(SCRI) SCRIIPS RES INST.	
PI	De la Torre JC;	
XX	WPI; 1998-398802/34.	
DR	New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.	
FT	New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.	
PT	New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.	
XX	Claim 5; Page 165; 207pp; English.	
PS	This peptide is characteristic of novel p40 proteins (see AAW49051-53) of human Borna disease virus (BDV) isolates obtained from psychiatric patients. The invention provides nucleic acids (see AAW49051-53) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain poly:peptides (see AAW49043-63) obtained from psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV poly:peptides. Human BDV poly:peptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)	
CC	This peptide is characteristic of novel p40 proteins (see AAW49051-53) of human Borna disease virus (BDV) isolates obtained from psychiatric patients. The invention provides nucleic acids (see AAW49051-53) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain poly:peptides (see AAW49043-63) obtained from psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV poly:peptides. Human BDV poly:peptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)	

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 1.1865 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-39

Sequence: 1 MPKXRLVDDADAMEDD 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_AA_New.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep:.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep:.*
4: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB pep:.*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB pep:.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep:.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep:.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	48.4	156	US-10-821-234-939	Sequence 939, App
2	40	42.1	375	US-11-051-267-2	Sequence 2, Appli
3	40	42.1	375	US-11-051-267-10	Sequence 10, Appl
4	40	42.1	375	US-11-051-267-14	Sequence 14, Appl
5	40	42.1	375	US-11-051-267-16	Sequence 16, Appl
6	40	42.1	376	US-11-051-267-4	Sequence 4, Appli
7	40	42.1	376	US-11-051-267-6	Sequence 6, Appli
8	40	42.1	491	US-10-954-468-54	Sequence 54, Appl
9	40	42.1	729	US-10-954-468-53	Sequence 53, Appl
10	40	42.1	732	US-10-954-468-51	Sequence 51, Appl
11	40	42.1	892	US-10-507-275-3	Sequence 3, Appli
12	40	42.1	904	US-10-507-275-5	Sequence 5, Appli
13	40	42.1	904	US-11-087-227-12	Sequence 12, Appl
14	40	42.1	970	US-10-954-468-52	Sequence 52, Appl
15	39.5	41.6	229	US-10-689-742-38	Sequence 38, Appl
16	39.5	41.6	262	US-10-689-742-65	Sequence 65, Appl
17	39	41.1	237	US-10-454-437-310	Sequence 310, App
18	39	41.1	421	US-10-131-826A-302	Sequence 302, App
19	38	40.0	35	US-10-467-657-5682	Sequence 5682, Ap
20	38	40.0	190	US-11-140-930-19	Sequence 19, Appl
21	38	40.0	540	US-10-858-730-293	Sequence 293, App
22	38	40.0	747	US-11-018-018-1	Sequence 1, Appli
23	38	40.0	747	US-11-047-757-1	Sequence 1, Appli
24	37	38.9	3507	US-11-075-185-7	Sequence 7, Appli
25	37	38.9	7968	US-11-143-980-49	Sequence 49, Appl

26	36.5	38.4	317	6	US-10-821-234-1388	Sequence 1388, Ap
27	36.5	38.4	407	6	US-10-821-234-1389	Sequence 1389, Ap
28	36.5	38.4	464	6	US-10-689-742-164	Sequence 164, App
29	36	37.9	15	7	US-11-106-932-53	Sequence 53, Appl
30	36	37.9	31	7	US-11-106-932-3	Sequence 3, Appli
31	36	37.9	222	6	US-10-467-657-20	Sequence 20, Appl
32	36	37.9	222	6	US-10-467-657-6182	Sequence 6182, Ap
33	36	37.9	228	6	US-10-883-512-70	Sequence 70, Appl
34	36	37.9	228	6	US-10-883-512-104	Sequence 104, App
35	36	37.9	228	6	US-10-883-512-104	Sequence 104, App
36	36	37.9	238	6	US-10-467-657-8350	Sequence 8350, App
37	36	37.9	348	6	US-10-467-657-8350	Sequence 8350, App
38	36	37.9	373	6	US-10-658-730-20	Sequence 20, Appl
39	36	37.9	374	7	US-11-051-267-8	Sequence 8, Appli
40	36	37.9	375	7	US-11-051-267-18	Sequence 18, Appli
41	36	37.9	399	6	US-10-821-234-1031	Sequence 1031, Ap
42	36	37.9	417	6	US-10-821-234-1536	Sequence 1536, Ap
43	36	37.9	468	7	US-11-054-385-12	Sequence 12, Appl
44	36	37.9	2261	6	US-10-995-561-600	Sequence 600, App
45	36	37.9	2261	6	US-10-511-545-1	Sequence 1, Appli

ALIGNMENTS

```

RESULT 1
US-10-821-234-939
; Sequence 939, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Scache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 939
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-939

Query Match      48.4% Score 46; DB 6; Length 156;
Best Local Similarity 75.0%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 RRLVDDADAMED 16
      |||||
Db      78 RRLVDDTDAASN 89

RESULT 2
US-11-051-267-2
; Sequence 2, Application US/11051267
; Publication No. US20050257278A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Alexandra C.
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/11/051,267
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 11.1994 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95

Sequence: 1 MPKRRRLVDADAMEDD 18

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA Main:

1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	US-10-627-141-39	Sequence 39, Appli
2	83	87.4	18	US-10-805-220-3	Sequence 3, Appli
3	50	52.6	740	US-10-437-963-196227	Sequence 196227,
4	49	51.6	466	US-10-437-963-136707	Sequence 136707,
5	49	51.6	1011	US-10-437-963-140426	Sequence 140426,
6	48.5	51.1	567	US-10-369-493-22125	Sequence 22125, A
7	48	50.5	707	US-10-425-115-217129	Sequence 217129,
8	48	50.5	736	US-10-425-114-6450	Sequence 46450, A
9	48	50.5	736	US-10-425-114-65891	Sequence 65891, A
10	48	50.5	1526	US-10-450-763-36475	Sequence 36475, A
11	48	50.5	1554	US-10-450-763-37647	Sequence 37647, A
12	48	50.5	1584	US-10-450-763-37649	Sequence 37649, A
13	48	50.5	1627	US-10-450-763-36476	Sequence 36476, A
14	48	50.5	1881	US-09-998-425-3	Sequence 3, Appli
15	48	50.5	1881	US-09-997-977-3	Sequence 3, Appli
16	48	50.5	430	US-10-424-599-166800	Sequence 166800,
17	47	49.4	131	US-09-989-722-276	Sequence 276, App
18	46	48.4	131	US-09-989-723-276	Sequence 276, App
19	46	48.4	131	US-09-989-727-276	Sequence 276, App
20	46	48.4	131	US-09-989-727-276	Sequence 276, App
21	46	48.4	131	US-09-989-731-276	Sequence 276, App
22	46	48.4	131	US-09-989-732-276	Sequence 276, App
23	46	48.4	131	US-09-991-073-276	Sequence 276, App
24	46	48.4	131	US-09-990-442-276	Sequence 276, App
25	46	48.4	131	US-09-991-163-276	Sequence 276, App
26	46	48.4	131	US-09-993-604-276	Sequence 276, App
27	46	48.4	131	US-09-993-604-276	Sequence 276, App

28	46	48.4	131	US-09-990-456-276	Sequence 276, App
29	46	48.4	131	US-09-989-721-276	Sequence 276, App
30	46	48.4	131	US-09-992-598-276	Sequence 276, App
31	46	48.4	131	US-09-989-293A-276	Sequence 276, App
32	46	48.4	131	US-09-989-735-276	Sequence 276, App
33	46	48.4	131	US-09-990-444-276	Sequence 276, App
34	46	48.4	131	US-09-991-181-276	Sequence 276, App
35	46	48.4	131	US-09-989-730-276	Sequence 276, App
36	46	48.4	131	US-09-990-438-276	Sequence 276, App
37	46	48.4	131	US-09-993-687-276	Sequence 276, App
38	46	48.4	131	US-09-989-734-276	Sequence 276, App
39	46	48.4	131	US-09-997-653-276	Sequence 276, App
40	46	48.4	131	US-09-989-724-276	Sequence 276, App
41	46	48.4	131	US-09-989-728-276	Sequence 276, App
42	46	48.4	131	US-09-990-441-276	Sequence 276, App
43	46	48.4	131	US-09-993-667-276	Sequence 276, App
44	46	48.4	131	US-09-997-428-276	Sequence 276, App
45	46	48.4	131	US-09-997-666-276	Sequence 276, App

ALIGNMENTS

RESULT 1
US-10-627-141-39
Sequence 39, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitching, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-627-141-39
Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MPKRRRLVDADAMEDD 18

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 3.1254 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-39

Sequence: 1 MPKRRLVDDADAMEDQD 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/laa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/laa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/laa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	2	US-08-779-764A-39 Sequence 39, Appl
2	95	100.0	18	2	US-09-563-456-39 Sequence 39, Appl
3	95	100.0	370	2	US-08-369-822C-2 Sequence 2, Appl
4	95	100.0	370	2	US-08-582-776C-2 Sequence 2, Appl
5	95	100.0	370	2	US-08-434-831B-2 Sequence 2, Appl
6	48	50.5	1881	2	US-09-233-086-3 Sequence 3, Appl
7	46	48.4	131	2	US-09-839-709-2 Sequence 2, Appl
8	46	48.4	131	2	US-09-991-181-276 Sequence 276, Appl
9	46	48.4	131	2	US-09-990-444-276 Sequence 276, Appl
10	46	48.4	131	2	US-09-997-333-276 Sequence 276, Appl
11	46	48.4	131	2	US-09-992-598-276 Sequence 276, Appl
12	43.5	45.8	314	1	US-08-989-478-4 Sequence 4, Appl
13	43.5	45.8	314	2	US-08-996-685-4 Sequence 4, Appl
14	41	43.2	41	2	US-09-314-268-101 Sequence 101, Appl
15	41	43.2	291	2	US-09-252-991A-25517 Sequence 25517, A
16	41	43.2	341	2	US-09-991-181-297 Sequence 297, Appl
17	41	43.2	341	2	US-09-990-444-297 Sequence 297, Appl
18	41	43.2	341	2	US-09-997-333-297 Sequence 297, Appl
19	41	43.2	341	2	US-09-992-598-297 Sequence 297, Appl
20	41	43.2	342	2	US-09-252-991A-27223 Sequence 27223, A
21	41	43.2	444	2	US-09-583-110-2893 Sequence 2893, Ap
22	41	43.2	466	2	US-09-107-433-3766 Sequence 3766, Ap
23	41	43.2	475	2	US-10-104-047-2925 Sequence 2925, Ap
24	41	43.2	481	2	US-09-489-039A-10323 Sequence 10323, A
25	41	43.2	1066	2	US-09-252-991A-31530 Sequence 31530, A
26	41	43.2	1136	2	US-09-252-991A-31394 Sequence 31394, A
27	40.5	42.6	1318	2	US-10-237-551-197 Sequence 197, App

28	40	42.1	70	2	US-09-640-211A-760 Sequence 760, App
29	40	42.1	195	2	US-09-270-767-46801 Sequence 46801, A
30	40	42.1	375	1	US-08-525-596B-14 Sequence 14, Appl
31	40	42.1	375	1	US-08-765-875-5 Sequence 5, Appl
32	40	42.1	375	2	US-08-795-671-5 Sequence 5, Appl
33	40	42.1	375	2	US-09-177-860A-14 Sequence 14, Appl
34	40	42.1	375	2	US-09-252-1498-29 Sequence 29, Appl
35	40	42.1	375	2	US-09-252-1498-30 Sequence 30, Appl
36	40	42.1	375	2	US-09-252-1498-32 Sequence 32, Appl
37	40	42.1	375	2	US-09-252-1498-33 Sequence 33, Appl
38	40	42.1	375	2	US-09-378-238-14 Sequence 14, Appl
39	40	42.1	375	2	US-09-451-501-19 Sequence 19, Appl
40	40	42.1	375	2	US-09-451-501-19 Sequence 19, Appl
41	40	42.1	375	2	US-09-629-938-14 Sequence 14, Appl
42	40	42.1	375	2	US-09-454-540-5 Sequence 5, Appl
43	40	42.1	375	2	US-09-686-344-14 Sequence 14, Appl
44	40	42.1	375	2	US-09-686-344-19 Sequence 19, Appl
45	40	42.1	375	2	US-09-686-344-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-779-764A-39
Sequence 39, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9398
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-779-764A-39
Query Match 100.0%; Score 95; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPKRRLVDDADAMEDQD 18
Db 1 MPKRRLVDDADAMEDQD 18

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 1.73633 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95

Sequence: 1 MPPKRLVDDADAMDDQD 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	370	2	A49528
2	48.5	51.1	567	2	S50708
3	45	47.4	326	2	A41855
4	43.5	45.8	314	2	A44437
5	43.5	45.8	457	2	S50357
6	43.5	45.8	567	2	S49600
7	43	45.3	302	1	T43822
8	43	45.3	302	2	B84322
9	43	45.3	388	2	AE0421
10	43	45.3	463	2	G75429
11	43	45.3	472	2	T45219
12	43	45.3	790	2	T19683
13	42	44.2	296	2	F70879
14	42	44.2	368	2	T47894
15	42	44.2	425	2	T16433
16	42	44.2	427	2	S19338
17	42	44.2	447	2	T66146
18	42	44.2	559	2	T19444
19	42	44.2	812	2	T34180
20	42	44.2	1287	2	T22235
21	42	44.2	1319	2	S75705
22	41	43.2	266	2	B84292
23	41	43.2	293	2	T22385
24	41	43.2	304	1	R3H835
25	41	43.2	411	2	H83355
26	41	43.2	444	2	E95065
27	41	43.2	578	2	T48795
28	41	43.2	754	2	T25551
29	41	43.2	780	2	T37456

30	41	43.2	902	2	T00072	hypothetical prote
31	40	42.1	127	2	T16131	hypothetical prote
32	40	42.1	186	2	T03808	alanine-tRNA ligase
33	40	42.1	223	2	A29770	cerbellar degene
34	40	42.1	307	2	S16622	stage III sporulat
35	40	42.1	414	2	T33878	hypothetical prote
36	40	42.1	469	2	A83411	hypothetical prote
37	40	42.1	469	2	S69640	hypothetical prote
38	40	42.1	501	2	S34825	uvr2 protein - Neu
39	40	42.1	546	2	T32382	hypothetical prote
40	40	42.1	601	2	A82561	hypothetical prote
41	40	42.1	783	2	T37457	Tricorn proteinase
42	40	42.1	799	2	C86287	P91.24 protein -
43	40	42.1	830	1	B46723	replication licens
44	40	42.1	868	1	S45757	replication licens
45	40	42.1	881	2	T26498	hypothetical prote

ALIGNMENTS

RESULT 1

A49528 probable structural component p40 - borna disease virus

N:Alternate names: 39k antigen

C:Species: borna disease virus

C>Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #ext_change 28-Jul-2000

C/Accession: A49528; A37475; S25642; A44004

R/Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A>Title: Sequence conservation in field and experimental isolates of Borna disease virus

A/Reference number: A49528; PMID:94076462; PMID:8254777

A/Accession: A49528

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-370 <SCH>

A/Cross-references: UNIPARC:UPI000017106E; GB:S67502; NID:9456883; PIDD:AMB29214.1; PII

A/Experimental source: WT-1, Halle BJ/91, horse brain, field isolate

A/Note: sequence extracted from NCBI backbone (NCBIN:141399, NCBIPI:141401)

R/Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A>Title: Genomic organization of the structural proteins of borna disease virus reveal

A/Reference number: A37475; PMID:9303922; PMID:8317098

A/Accession: A37475

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A/Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:9386390; PIDD:AMB27261.1; PII

A/Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBIPI:134147)

R/Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A/Description: The 39/39k antigen of borna disease virus.

A/Reference number: S25642

A/Accession: S25642

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A/Cross-references: UNIPARC:UPI0000170E05; EMBL:X68392; NID:958687; PIDD:CAA48458.1; P

J. Virol. 66, 6572-6577, 1992

A>Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w

A/Reference number: A44004; PMID:93021385; PMID:1404604

A/Accession: A44004

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 14-46, 'T', 48-55, 'T', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A/Cross-references: UNIPARC:UPI0000170E06; GB:M99375; NID:9210698; PIDD:AAA73385.1; P

C/Superfamily: borna disease virus p40

Query Match 100.0%; Score 95; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 17, 2006, 15:28:28 ; Search time 11.9228 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95
Sequence: 1 MPPKRLVDADAMEDQD 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003s:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	2 AAW49061	AAW49061 Human Bor
2	95	100.0	370	2 AAR98617	AAR98617 Borna dis
3	83	87.4	18	AD575684	AD575684 Borna dis
4	48.5	51.1	567	AD543695	AD543695 Bacterial
5	48	50.5	345	9 AEB27254	AEB27254 Plasmid
6	48	50.5	736	8 ADY10076	ADY10076 Plant ful
7	48	50.5	736	8 ADX77084	ADX77084 Plant ful
8	48	50.5	1134	7 ADE61439	ADE61439 Human pro
9	48	50.5	1526	4 AAM79777	AAM79777 Human pro
10	48	50.5	1526	4 ABG06116	ABG06116 Novel hum
11	48	50.5	1526	4 ABG07289	ABG07289 Novel hum
12	48	50.5	1552	4 AAM78793	AAM78793 Human pro
13	48	50.5	1554	4 ABG07288	ABG07288 Novel hum
14	48	50.5	1584	4 ABG07290	ABG07290 Novel hum
15	48	50.5	1627	4 ABG06117	ABG06117 Novel hum
16	48	50.5	1881	2 AAY24025	AAY24025 Amlnb act
17	46	48.4	131	3 AAY6712	AAY6712 Membrane-
18	46	48.4	131	3 AAY57844	AAY57844 Human lep
19	46	48.4	131	3 AAB03730	AAB03730 OB-RGRP2
20	46	48.4	131	3 AAY94849	AAY94849 Human pro
21	46	48.4	131	4 AAU29127	AAU29127 Human PRO
22	46	48.4	131	4 AAB88337	AAB88337 Human mem
23	46	48.4	131	4 AAB65235	AAB65235 Human PRO
24	46	48.4	131	5 ABB89581	ABB89581 Human pol

25	46	48.4	131	5 ABB84894	ABB84894 Human PRO
26	46	48.4	131	5 ABB95500	ABB95500 Human ang
27	46	48.4	131	5 ABB58503	ABB58503 Human PRO
28	46	48.4	131	6 ABB88051	ABB88051 Novel hum
29	46	48.4	131	6 ABB84366	ABB84366 Human sec
30	46	48.4	131	6 ABB66240	ABB66240 Human sec
31	46	48.4	131	6 ABB65630	ABB65630 Human sec
32	46	48.4	131	6 ABB99570	ABB99570 Human sec
33	46	48.4	131	6 ABB58050	ABB58050 Human PRO
34	46	48.4	131	6 ABB59128	ABB59128 Novel hum
35	46	48.4	131	6 ABB82640	ABB82640 Human sec
36	46	48.4	131	6 ABB82809	ABB82809 Human PRO
37	46	48.4	131	6 ABB99930	ABB99930 Novel hum
38	46	48.4	131	6 ABB68179	ABB68179 Human sec
39	46	48.4	131	6 ABB60559	ABB60559 Human sec
40	46	48.4	131	6 ABB96232	ABB96232 Novel hum
41	46	48.4	131	6 ABB92663	ABB92663 Human sec
42	46	48.4	131	6 ABB08740	ABB08740 Human sec
43	46	48.4	131	6 ABB002792	ABB002792 Human sec
44	46	48.4	131	6 ABB74946	ABB74946 Human sec
45	46	48.4	131	6 ABB94708	ABB94708 Human sec

ALIGNMENTS

RESULT 1
ID AAW49061
AAW49061 standard; peptide; 18 AA.

AC AAW49061;
XX XX
XX XX
DT 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
XX XX
XX XX
DE Human Borna disease virus p40 peptide.
XX XX
XX XX
KW BDV; infection; diagnosis; neuropsychiatric disorder; human.
OS Borna disease virus.
XX XX
XX XX
PN WO9830238-A1.
XX XX
PD 16-JUL-1998.
XX XX
PF 07-JAN-1998; 98WO-US000495.
XX XX
PR 07-JAN-1997; 9TUS-00779764.
XX XX
PA (SCRI) SCRIPPS RES INST.
XX XX
PI De La Torre JC;
XX XX
DR WPI; 1998-398802/34.
XX XX
PT New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly-peptide(s), used to develop products for detection.
XX XX
XX XX
XX Claim 5; Page 165; 207pp; English.

This peptide is characteristic of novel p40 proteins (see AAW49051-53) of human Borna disease virus (BDV) isolates obtained from psychiatric patients. The invention provides nucleic acids (see AAW32840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain poly-peptides (see AAW49043-63) obtained from psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV poly-peptides. Human BDV poly-peptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 12.4582 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975

Sequence: 1 HTVPSLVFCLIPGLHAA.....TTIKYVLAECMDATLTPV 189

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76.5	7.8	246	US-11-054-515-1393	Sequence 1393, Ap
2	76.5	7.8	249	US-11-054-515-1347	Sequence 1347, Ap
3	73	7.5	151	US-10-793-626-1646	Sequence 1646, Ap
4	72.5	7.4	1474	US-10-995-561-873	Sequence 873, App
5	70.5	7.2	753	US-10-858-730-225	Sequence 225, App
6	70	7.2	456	US-11-074-176-238	Sequence 238, App
7	68	7.0	181	US-10-467-657-8084	Sequence 8084, Ap
8	67.5	6.9	249	US-11-054-515-1296	Sequence 1296, Ap
9	67.5	6.9	884	US-10-878-556A-9	Sequence 9, Appl
10	67.5	6.9	974	US-10-821-234-1152	Sequence 1152, Ap
11	67	6.9	374	US-10-517-939-356	Sequence 356, Appl
12	67	6.9	1114	US-11-174-150-35	Sequence 35, Appl
13	66.5	6.8	247	US-11-000-463-242	Sequence 242, App
14	66.5	6.8	350	US-11-082-389-380	Sequence 380, App
15	66	6.8	251	US-11-054-515-1669	Sequence 1669, App
16	66	6.8	300	US-10-793-626-1900	Sequence 1900, Ap
17	66	6.8	308	US-10-793-626-1732	Sequence 1732, Ap
18	66	6.8	374	US-10-517-939-340	Sequence 340, App
19	65.5	6.7	442	US-10-467-657-1614	Sequence 1614, App
20	65	6.7	158	US-11-074-176-326	Sequence 326, App
21	65	6.7	172	US-11-074-176-94	Sequence 94, Appl
22	65	6.7	240	US-10-821-234-1003	Sequence 1003, App
23	64.5	6.6	864	US-11-194-246-343	Sequence 343, App
24	64.5	6.6	210	US-10-793-626-2864	Sequence 2864, Ap
25	64.5	6.6	210	US-10-793-626-3320	Sequence 3320, Ap

26	64	6.6	854	US-10-511-657-4	Sequence 4, Appl
27	63	6.5	232	US-11-055-822-848	Sequence 848, App
28	63	6.5	257	US-11-054-515-1033	Sequence 1033, Ap
29	62.5	6.4	406	US-10-821-234-1521	Sequence 1521, Ap
30	62.5	6.4	572	US-10-454-437-68	Sequence 68, Appl
31	62.5	6.4	584	US-10-454-437-66	Sequence 66, Appl
32	62.5	6.4	795	US-10-821-234-1675	Sequence 1675, Ap
33	62.5	6.4	1141	US-10-601-368-6	Sequence 6, Appl
34	62.5	6.4	1166	US-10-601-368-4	Sequence 4, Appl
35	62.5	6.4	1188	US-10-601-368-3	Sequence 3, Appl
36	62.5	6.4	1188	US-11-000-463-338	Sequence 338, App
37	62.5	6.4	1188	US-11-000-463-810	Sequence 810, App
38	61.5	6.3	391	US-10-613-744-13	Sequence 13, Appl
39	61.5	6.3	623	US-10-873-528-88	Sequence 88, Appl
40	61.5	6.3	993	US-10-055-877-6	Sequence 6, Appl
41	61	6.3	249	US-11-054-515-1445	Sequence 1445, Ap
42	61	6.3	249	US-11-054-515-1641	Sequence 1641, Ap
43	61	6.3	253	US-11-054-515-1242	Sequence 1242, Ap
44	61	6.3	253	US-11-054-515-1298	Sequence 1298, Ap
45	61	6.3	255	US-11-054-515-1281	Sequence 1281, Ap

ALIGNMENTS

RESULT 1
US-11-054-515-1393
Sequence 1393, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1393
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1393
Query Match 7.8%; Score 76.5; DB 7; Length 246;
Best Local Similarity 24.8%; Pred. No. 0.57;
Matches 28; Conservative 19; Mismatches 39; Indels 27; Gaps 7;
Query 86 IKAGADIKRRKPTMAALRPDSHGRTTLQMPNPKRAIDWT-----NQCPVGSRYLS 140
DB 5 VQSGAR-VKPPGSSVAVKVC-KASGDN-----FNSY-AISWQAGQGPENWGGRIPV 54
Query 141 LITTFESPKERFMDQIKIVASYAQMNTTYTIKE-----YLAECMDATL 184

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 117.593 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975
Sequence: 1 HTVPSLIVLCILIPGLHA.....TTIKYLACMDATITPVV 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*
1: /cgn2_6/pcodara/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/pcodara/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/pcodara/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/pcodara/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/pcodara/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/pcodara/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	975	100.0	189	4 US-10-627-141-30	Sequence 30, Appl
2	969	99.4	189	4 US-10-627-141-28	Sequence 28, Appl
3	960	98.5	189	4 US-10-627-141-29	Sequence 29, Appl
4	328.5	33.7	273	5 US-10-128-558-370	Sequence 370, Appl
5	311	31.9	272	5 US-10-128-558-185	Sequence 185, Appl
6	94.5	9.7	1350	4 US-10-437-963-125423	Sequence 125423, Appl
7	92.5	9.5	940	4 US-10-437-963-197289	Sequence 197289, Appl
8	90	9.2	129	4 US-10-424-599-237276	Sequence 237276, Appl
9	90	9.2	238	4 US-10-291-190-25	Sequence 25, Appl
10	89.5	9.2	2225	6 US-11-097-143-42423	Sequence 42423, A
11	88.5	9.1	1186	4 US-10-437-963-197319	Sequence 197319, A
12	87	8.9	270	4 US-10-425-114-56047	Sequence 56047, A
13	87	8.9	396	4 US-10-425-114-43995	Sequence 43995, A
14	87	8.9	585	4 US-10-424-599-237273	Sequence 237273, A
15	85	8.7	82	3 US-09-796-692-2393	Sequence 2393, Appl
16	85	8.7	82	4 US-10-040-862-2393	Sequence 2393, Appl
17	85	8.7	82	4 US-10-057-4758-2393	Sequence 2393, Appl
18	85	8.7	82	4 US-10-154-8848-2393	Sequence 2393, Appl
19	85	8.7	82	4 US-10-764-324-2393	Sequence 2393, Appl
20	85	8.7	1159	4 US-10-437-963-129387	Sequence 129387, A
21	84.5	8.6	304	6 US-11-021-619-22	Sequence 22, Appl
22	83.5	8.6	1959	4 US-10-437-963-154458	Sequence 154458, A
23	82.5	8.5	870	4 US-10-437-963-154457	Sequence 154457, A
24	81.5	8.4	1190	6 US-11-097-143-14232	Sequence 14232, A
25	81.5	8.4	2076	4 US-10-437-963-197291	Sequence 197291, A
26	80.5	8.3	1205	4 US-10-437-963-197324	Sequence 197324, A
27	79.5	8.2	1278	4 US-10-437-963-181016	Sequence 181016, A

28	79	8.1	782	6 US-11-097-143-297	Sequence 297, Appl
29	78.5	8.1	1389	4 US-10-437-963-129393	Sequence 129393, A
30	78.5	8.1	2393	4 US-10-437-963-197261	Sequence 197261, A
31	78	8.0	620	4 US-10-282-122A-64220	Sequence 64220, A
32	78	8.0	1346	4 US-10-437-963-189131	Sequence 189131, A
33	77.5	7.9	603	4 US-10-425-114-67123	Sequence 67123, A
34	77.5	7.9	609	4 US-10-425-115-274794	Sequence 274794, A
35	77.5	7.9	937	4 US-10-437-963-197334	Sequence 197334, A
36	77.5	7.9	1293	4 US-10-437-963-129354	Sequence 129354, A
37	77	7.9	353	4 US-10-282-122A-74877	Sequence 74877, A
38	77	7.9	420	4 US-10-094-749-2235	Sequence 2235, Appl
39	77	7.9	481	3 US-09-955-999-104	Sequence 104, Appl
40	77	7.9	527	4 US-10-437-963-203871	Sequence 203871, A
41	77	7.9	593	5 US-10-732-923-9500	Sequence 9500, Appl
42	77	7.9	847	4 US-10-478-245-7	Sequence 7, Appl
43	76.5	7.8	246	3 US-09-880-748-1393	Sequence 1393, Appl
44	76.5	7.8	246	4 US-10-293-418-1393	Sequence 1393, Appl
45	76.5	7.8	249	3 US-09-880-748-1347	Sequence 1347, Appl

ALIGNMENTS

```
RESULT 1
US-10-627-141-30
; Sequence 30, Application US/106277141
; Publication No. US20040162421A1
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,141
; FILING DATE: 25-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764
; FILING DATE: 16-Dec-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Filting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-627-141-30
Query Match 100.0%; Score 975; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 5.5e-102;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HTVPSLIVLCILIPGLHAFAHGVGRSYSTPTREGRVYVTKAKYGGKTTORDLT 60
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 32.8167 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975
Sequence: 1 HTVPSLVFCLIPGLHAA.....TTIKVLAECMDATLTIPV 189

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pap:*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pap:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pap:*
- 4: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pap:*
- 5: /cgn2_6/ptodata/1/1aa/RB_COMB.pap:*
- 6: /cgn2_6/ptodata/1/1aa/backfill1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	189	2	US-08-779-764A-30 Sequence 30, Appl
2	975	100.0	189	2	US-09-563-456-30 Sequence 30, Appl
3	974	99.9	370	2	US-08-369-822C-2 Sequence 2, Appl
4	974	99.9	370	2	US-08-582-776C-2 Sequence 2, Appl
5	974	99.9	370	2	US-08-434-831B-2 Sequence 2, Appl
6	969	99.4	189	2	US-08-779-764A-28 Sequence 28, Appl
7	969	99.4	189	2	US-09-563-456-28 Sequence 28, Appl
8	960	98.5	189	2	US-08-779-764A-29 Sequence 29, Appl
9	960	98.5	189	2	US-09-563-456-29 Sequence 29, Appl
10	76.5	7.8	409	2	US-09-270-767-42348 Sequence 42348, A
11	76.5	7.8	1919	2	US-10-152-886-13 Sequence 13, Appl
12	76	7.8	534	1	US-08-577-184-2 Sequence 2, Appl
13	75	7.7	761	2	US-09-328-352-5650 Sequence 5650, Ap
14	74.5	7.6	519	2	US-09-134-000C-4482 Sequence 4482, Ap
15	74	7.6	470	2	US-09-252-991A-25558 Sequence 25558, A
16	73.5	7.5	211	2	US-09-543-681A-6708 Sequence 6708, Ap
17	73.5	7.5	346	2	US-09-724-224-6 Sequence 6, Appl
18	73.5	7.5	346	2	US-10-093-317-6 Sequence 6, Appl
19	73.5	7.5	370	2	US-09-724-224-2 Sequence 2, Appl
20	73.5	7.5	370	2	US-10-093-317-2 Sequence 2, Appl
21	73.5	7.5	487	2	US-09-724-224-8 Sequence 8, Appl
22	73.5	7.5	487	2	US-10-093-317-8 Sequence 8, Appl
23	73.5	7.5	490	2	US-09-949-016-8784 Sequence 8784, Ap
24	73.5	7.5	512	2	US-09-724-224-4 Sequence 4, Appl
25	73.5	7.5	512	2	US-10-093-317-4 Sequence 4, Appl
26	73.5	7.5	568	2	US-09-489-039A-13755 Sequence 13755, A
27	73.5	7.5	665	2	US-09-595-684B-35 Sequence 35, Appl

28	73.5	7.5	859	2	US-09-902-540-14220 Sequence 14220, A
29	73	7.5	151	2	US-09-710-279-1646 Sequence 1646, Ap
30	73	7.5	154	2	US-09-134-001C-4123 Sequence 4123, Ap
31	72.5	7.4	1219	2	US-09-107-532A-6020 Sequence 6020, Ap
32	72.5	7.4	1474	2	US-09-241-606-2 Sequence 2, Appl
33	72.5	7.4	1474	2	US-09-949-002-287 Sequence 287, Appl
34	72.5	7.4	1491	2	US-09-949-002-434 Sequence 434, Appl
35	72	7.4	440	2	US-09-591-095-27 Sequence 27, Appl
36	72	7.4	488	2	US-09-540-236-3027 Sequence 3027, Ap
37	72	7.4	1695	2	US-09-866-108A-15753 Sequence 15753, A
38	71.5	7.3	427	2	US-09-489-039A-12852 Sequence 12852, A
39	71	7.3	946	4	PCT-US95-08493-13 Sequence 13, Appl
40	71	7.3	2522	2	US-09-251-645-13 Sequence 13, Appl
41	70.5	7.2	387	1	US-08-123-161A-10 Sequence 10, Appl
42	70.5	7.2	387	1	US-08-483-278-10 Sequence 10, Appl
43	70.5	7.2	456	2	US-09-949-016-9294 Sequence 9294, Ap
44	70.5	7.2	465	2	US-09-328-352-4555 Sequence 4555, Ap
45	69.5	7.1	318	2	US-09-724-864-60 Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-779-764A-30
Sequence 30, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 NO. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2837
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-764A-30
Query Match 100.0%; Score 975; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.2e-111;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTVPSLVFCLIPGLHAAFGVGVRESYLSPTIRGEQTVVAKFYGEKTDQDLT 60
Db 1 HTVPSLVFCLIPGLHAAFGVGVRESYLSPTIRGEQTVVAKFYGEKTDQDLT 60
QY 61 ELAISSTFSCCLLIGVYIGSSSKIKAKGKQIKKFKTMALNPSHETATLQWEN 120

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 18.2315 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975
Sequence: 1 HTVPSLVPLCLIPGLHAA.....TTIKVLAECMDATITIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	99.9	370	A49528	probable structural
2	86	8.8	448	A11659	DNA repair protein
3	81.5	8.4	200	C41873	heat shock protein
4	81.5	8.4	200	A97058	molecular chaperon
5	79	8.1	1021	T42634	connectin/chaperon
6	78.5	8.1	352	A69743	ATP-binding Mip-1i
7	78	8.0	620	S73809	DNA primase - Myco
8	76.5	7.8	337	A10061	hypothetical prote
9	76.5	7.8	350	AC0813	ethanolamine obero
10	76.5	7.8	592	E75032	carbon starvation
11	76	7.8	408	T32237	hypothetical prote
12	76	7.8	433	S05654	ND3 fusion protein
13	76	7.8	849	S77217	phosphorylase (EC
14	76	7.7	2123	S55089	probable acetyl-Co
15	75.5	7.7	389	SYPCF	naringenin-chalcon
16	75.5	7.7	493	C71903	D-alanyl-D-alanine
17	75	7.7	1252	B42771	reticulocyte-bind
18	74.5	7.6	311	AH2153	hypothetical prote
19	74.5	7.6	329	H71132	hypothetical prote
20	74.5	7.6	457	G82187	biopolymer transpo
21	74	7.6	427	D83347	probable aminotran
22	73.5	7.5	500	T19565	hypothetical prote
23	73.5	7.5	274	C72276	phosphate ABC tran
24	73.5	7.5	383	H86232	hypothetical prote
25	73.5	7.5	920	T11052	antipeptidase (EC
26	73	7.5	233	B61222	cytochrome-c oxida
27	73	7.5	388	T36766	probable two-compo
28	73	7.5	507	B89792	hypothetical prote
29	73	7.5	908	S51293	probable membrane

30	72.5	7.4	330	2	T49002	hypothetical prote
31	72.5	7.4	662	2	C54078	methyl-accepting c
32	72.5	7.4	753	2	B86070	terahydropteroylt
33	72.5	7.4	753	2	G91223	terahydropteroylt
34	72.5	7.4	1474	1	MAHU	alpha-2-macroglobu
35	72.5	7.4	2180	2	A46182	polypotein - echo
36	72	7.4	335	2	AB0983	probable lact-fam
37	72	7.4	351	2	T29369	hypothetical prote
38	72	7.4	666	2	S54401	penicillin-binding
39	72	7.4	678	2	AE0948	probable glycosyl
40	72	7.4	1224	2	T19749	hypothetical prote
41	71.5	7.4	1333	2	S65812	ABC transporter (A
42	71.5	7.3	300	2	AB1723	ATP-dependent heli
43	71.5	7.3	708	2	H82751	hypothetical prote
44	71.5	7.3	803	2	T00092	hypothetical prote
45	71.5	7.3	857	2	C97707	lipb protein limpo

ALIGNMENTS

RESULT 1

A49528 probable structural component p40 - borna disease virus

N/Alternate names: 39K antigen
C/Species: borna disease virus

C/Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text change 28-Jul-2000
C/Accession: A49528; A37475; S25642; A44004

R/Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.
J. Virol. 68, 63-68, 1994

A/Title: Sequence conservation in field and experimental isolates of Borna disease virus
A/Reference number: A49528; MUID:94076462; PMID:8254777

A/Accession: A49528
A/Status: preliminary
A/Molecule type: genomic RNA

A/Residues: 1-370 <SCG>
A/Cross-references: UNIPARC:UPI000017068; GB:S67502; NID:G456883; PIND:AB29214.1; P.

A/Experimental source: WT-1, Halle BL/91, horse brain, field isolate
A/Note: Sequence extracted from NCBI backbone (NCBIN:141399, NCBI:P:141401)

R/Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.
Virology 195, 229-238, 1993

A/Title: Genomic organization of the structural proteins of borna disease virus reveal.
A/Reference number: A37475; MUID:93303922; PMID:8317098

A/Accession: A37475
A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>
A/Cross-references: UNIPARC:UPI000017065; GB:S62821; NID:G386390; PIND:AB27261.1; P.

A/Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBI:P:134147)
A/Note: parts of this sequence were confirmed by peptide sequencing

R/Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,
submitted to The EMBL Data Library, September 1992

A/Description: The 39/39K antigen of borna disease virus.
A/Reference number: S25642

A/Accession: S25642
A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>
A/Cross-references: UNIPARC:UPI000017065; EMBL:X63392; NID:G58687; PIND:CAA48458.1; P.

R/McClure, M.A.; Thibault, K.J.; Hatalski, C.G.; Lipkin, W.I.
J. Virol. 66, 6572-6577, 1992

A/Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w.
A/Reference number: A44004; MUID:93021385; PMID:1404604

A/Accession: A44004
A/Status: preliminary
A/Molecule type: genomic RNA

A/Residues: 14-46, 'T', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>
A/Cross-references: UNIPARC:UPI000017066; GB:M99375; NID:G210698; PIND:AAA73385.1; P.

C/Superfamily: Borna disease virus p40

Query Match 99.9%; Score 974; DB 2; Length 370;
Best Local Similarity 99.5%; Pred. No. 8e-86;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds
(without alignment)

1176.511 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975

Sequence: 1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnIProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	190	2	065470_BDV
2	974	99.9	370	1	VP40_BDV
3	974	99.9	370	2	010355_BDV
4	974	99.9	370	2	010401_BDV
5	974	99.9	370	2	05GL86_BDV
6	974	99.9	370	2	05GL92_BDV
7	974	99.9	370	2	05GL95_BDV
8	974	99.9	370	2	05GLC8_BDV
9	974	99.9	370	2	05GLD1_BDV
10	974	99.9	370	2	08B829_BDV
11	974	99.9	370	2	0910H1_BDV
12	974	99.9	370	2	091UR4_BDV
13	974	99.9	370	2	091UR8_BDV
14	974	99.9	370	2	0774E9_BDV
15	973	99.8	370	2	010398_BDV
16	970	99.5	370	2	05GL98_BDV
17	969	99.4	190	2	05GL68_BDV
18	968	99.3	370	2	05GL50_BDV
19	968	99.3	370	2	05GL62_BDV
20	968	99.3	370	2	05GL71_BDV
21	968	99.3	370	2	05GLB3_BDV
22	967	99.2	369	2	09Q9V1_BDV
23	964	98.9	370	2	010392_BDV
24	960	98.5	190	2	065469_BDV
25	908	93.1	176	2	077A29_BDV
26	908	93.1	176	2	077A30_BDV
27	908	93.1	176	2	077A31_BDV
28	908	93.1	176	2	077A32_BDV
29	908	93.1	176	2	077A33_BDV
30	908	93.1	176	2	077A34_BDV
31	908	93.1	176	2	09W8R2_BDV

32	894	91.7	176	2	09W817_BDV	09W817 borna disea
33	782	80.2	152	2	09QCJ2_BDV	09QCJ2 borna disea
34	755	77.4	146	2	012852_BDV	012852 borna disea
35	755	77.4	146	2	012853_BDV	012853 borna disea
36	755	77.4	146	2	012855_BDV	012855 borna disea
37	755	77.4	146	2	012856_BDV	012856 borna disea
38	755	77.4	146	2	012857_BDV	012857 borna disea
39	755	77.4	146	2	012858_BDV	012858 borna disea
40	755	77.4	146	2	012859_BDV	012859 borna disea
41	755	77.4	146	2	012860_BDV	012860 borna disea
42	755	77.4	146	2	012861_BDV	012861 borna disea
43	755	77.4	146	2	012862_BDV	012862 borna disea
44	755	77.4	146	2	012863_BDV	012863 borna disea
45	755	77.4	146	2	012864_BDV	012864 borna disea

ALIGNMENTS

RESULT 1	ID	Query Match	Length	ID	Description
065470_BDV	065470_BDV	100.0%	190	2	065470 borna disea
065470_BDV	065470_BDV	100.0%	190	1	VP40_BDV
01-NOV-1996 (Tremblrel. 01, Created)	01-NOV-1996 (Tremblrel. 01, Last sequence update)	100.0%	190	2	010355_BDV
01-MAR-2004 (Tremblrel. 26, Last annotation update)	01-MAR-2004 (Tremblrel. 26, Last annotation update)	100.0%	190	2	010401_BDV
Borna disease virus (BDV)	Borna disease virus (BDV)	100.0%	190	2	05GL86_BDV
Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae; Bornavirus.	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae; Bornavirus.	100.0%	190	2	05GL92_BDV
NCBI_TaxID=12455;	NCBI_TaxID=12455;	100.0%	190	2	05GL95_BDV
NUCLEOTIDE SEQUENCE.	NUCLEOTIDE SEQUENCE.	100.0%	190	2	05GLC8_BDV
MEDLINE=97233300; PubMed=918344;	MEDLINE=97233300; PubMed=918344;	100.0%	190	2	05GLD1_BDV
Bode L.; Duerwald R.; Rantam P.A.; Perszt R.; Ludwig H.;	Bode L.; Duerwald R.; Rantam P.A.; Perszt R.; Ludwig H.;	100.0%	190	2	08B829_BDV
"First isolates of infectious human Borna disease virus from patients with mood disorders.";	"First isolates of infectious human Borna disease virus from patients with mood disorders.";	100.0%	190	2	0910H1_BDV
Mol. Psychiatry 1:200-212(1996).	Mol. Psychiatry 1:200-212(1996).	100.0%	190	2	091UR4_BDV
EMBL; U58596; F005244.1; -; Genomic RNA.	EMBL; U58596; F005244.1; -; Genomic RNA.	100.0%	190	2	091UR8_BDV
HSSP; Q01552; IN93.	HSSP; Q01552; IN93.	100.0%	190	2	0774E9_BDV
InterPro; IPR009441; BDV_P40.	InterPro; IPR009441; BDV_P40.	100.0%	190	2	010398_BDV
PANTHER; PTHR10207; BDV_P40; 1.	PANTHER; PTHR10207; BDV_P40; 1.	100.0%	190	2	05GL98_BDV
Pfam; PF06407; BDV_P40; 1.	Pfam; PF06407; BDV_P40; 1.	100.0%	190	2	05GL68_BDV
NOV_TER	NOV_TER	100.0%	190	2	05GL50_BDV
SEQUENCE	SEQUENCE	100.0%	190	2	05GL62_BDV
Query Match	Query Match	100.0%	190	2	05GL71_BDV
Best local similarity 100.0%; Pred. No. 9.1e-86;	Best local similarity 100.0%; Pred. No. 9.1e-86;	100.0%	190	2	05GLB3_BDV
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%	190	2	09Q9V1_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	010392_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	065469_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	077A29_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	077A30_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	077A31_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	077A32_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	077A33_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	077A34_BDV
1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	1 HTVPSLVFCLIPGHA...TTIKYLAECMDATITIPV 189	100.0%	190	2	09W8R2_BDV

RESULT 2	VP40_BDV	STANDARD;	PRT;	370 AA.
ID	VP40_BDV	STANDARD;	PRT;	370 AA.
AC	001552;	STANDARD;	PRT;	370 AA.
DT	01-JUL-1993 (Rel. 26, Created)	STANDARD;	PRT;	370 AA.

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 12.4582 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-29

Sequence: 1 HWTPSLVFLCLIPGLHMA.....TTIKXYLAECMDATLTPVY 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA New:
1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB pep:*
2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB pep:*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB pep:*
4: /cgn2_6/prodata/2/pubppa/PC9_NEW_PUB pep:*
5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB pep:*
6: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB pep:*
7: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB pep:*
8: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75.5	7.8	246	US-11-054-515-1393	Sequence 1393, App
2	75.5	7.8	249	US-11-054-515-1347	Sequence 1347, App
3	74.5	7.6	1474	US-10-995-561-873	Sequence 873, App
4	70	7.2	4655	US-10-995-561-556	Sequence 556, App
5	69.5	7.1	753	US-10-858-730-225	Sequence 225, App
6	68	7.0	158	US-11-074-176-326	Sequence 326, App
7	68	7.0	172	US-11-074-176-94	Sequence 94, App
8	68	7.0	249	US-11-054-515-1296	Sequence 1296, App
9	68	7.0	251	US-11-054-515-1669	Sequence 1669, App
10	68	7.0	456	US-11-074-176-238	Sequence 238, App
11	67.5	6.9	442	US-10-467-657-1614	Sequence 1614, App
12	66.5	6.8	151	US-10-793-626-1646	Sequence 1646, App
13	66.5	6.8	350	US-11-082-389-280	Sequence 380, App
14	65.5	6.7	356	US-11-052-554A-12	Sequence 12, App
15	65.5	6.7	572	US-10-454-437-68	Sequence 68, App
16	65.5	6.7	584	US-10-454-437-66	Sequence 66, App
17	65	6.7	240	US-10-821-234-1003	Sequence 1003, App
18	65	6.7	300	US-10-793-626-1900	Sequence 1900, App
19	65	6.7	364	US-11-087-177-33	Sequence 33, App
20	65	6.7	374	US-10-517-939-340	Sequence 340, App
21	65	6.7	871	US-10-933-025-3	Sequence 3, App
22	64.5	6.6	391	US-10-613-744-13	Sequence 13, App
23	64.5	6.6	539	US-10-514-250A-28	Sequence 28, App
24	64.5	6.6	539	US-10-514-250A-29	Sequence 29, App
25	64.5	6.6	539	US-10-514-250A-30	Sequence 30, App

26	64.5	6.6	539	US-10-514-250A-31	Sequence 31, App
27	64.5	6.6	539	US-10-514-250A-32	Sequence 32, App
28	64.5	6.6	539	US-10-514-250A-33	Sequence 33, App
29	64.5	6.6	539	US-10-514-250A-34	Sequence 34, App
30	64	6.6	374	US-10-517-939-356	Sequence 356, App
31	64	6.6	854	US-10-511-657-4	Sequence 4, App
32	63	6.5	359	US-10-055-877-265	Sequence 265, App
33	63	6.5	359	US-11-080-091-1	Sequence 1, App
34	63	6.5	359	US-11-116-939-15	Sequence 15, App
35	63	6.5	359	US-11-087-177-23	Sequence 23, App
36	63	6.5	359	US-11-087-177-25	Sequence 25, App
37	63	6.5	350	US-11-043-542-12	Sequence 12, App
38	63	6.5	364	US-11-087-177-31	Sequence 31, App
39	63	6.5	365	US-11-087-177-27	Sequence 27, App
40	63	6.5	367	US-11-043-542-10	Sequence 10, App
41	63	6.5	372	US-11-043-542-8	Sequence 8, App
42	63	6.5	373	US-11-043-542-14	Sequence 14, App
43	63	6.5	385	US-11-043-542-4	Sequence 4, App
44	63	6.5	385	US-11-043-542-6	Sequence 6, App
45	63	6.5	452	US-10-467-962B-14	Sequence 14, App

ALIGNMENTS

```

RESULT 1
US-11-054-515-1393
; Sequence 1393, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PR52P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1393
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1393
Query Match 7.8%; Score 75.5; DB 7; Length 246;
Best Local Similarity 22.5%; Pred. No. 0.88;
Matches 27; Conservative 17; Mismatches 43; Indels 33; Gaps 6;
QY 79 VIGSSKIKAEADQIKKFTTMAAVNRSHGETATLTFNPFHAIWT-----NCQPV 133
DB 4 LVQSGAEVKKPGSSVYKSCVA-----SGEN-----FNSY-AISWROAPGQGF 47
QY 134 VGSFVSLTLTTPDESQKEMDOIKLVAASAOQTYTTTKE-----YLAECMDATL 184

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 117.593 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974

Sequence: 1 HTWPSLVFCLIPGLHAA.....TTIKYLAECMDATLTPV 189

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	100.0	189	4 US-10-627-141-29	Sequence 29, Appl
2	960	98.6	189	4 US-10-627-141-30	Sequence 30, Appl
3	954	97.9	189	4 US-10-627-141-28	Sequence 28, Appl
4	329.5	33.8	273	5 US-10-128-558-370	Sequence 370, Appl
5	312	32.0	272	5 US-10-128-558-185	Sequence 185, Appl
6	96.5	9.9	940	4 US-10-437-963-197289	Sequence 197289, Appl
7	96.5	9.9	1350	4 US-10-437-963-125423	Sequence 125423, Appl
8	92.5	9.5	1186	4 US-10-437-963-197319	Sequence 197319, Appl
9	90	9.2	238	4 US-10-291-190-25	Sequence 25, Appl
10	85	8.7	82	3 US-09-796-692-2393	Sequence 2393, Appl
11	85	8.7	82	4 US-10-040-862-6393	Sequence 2393, Appl
12	85	8.7	82	4 US-10-057-475B-2393	Sequence 2393, Appl
13	85	8.7	82	4 US-10-154-884B-2393	Sequence 2393, Appl
14	85	8.7	82	4 US-10-764-324-2393	Sequence 2393, Appl
15	84.5	8.7	82	4 US-11-097-143-32423	Sequence 42423, Appl
16	83	8.5	129	4 US-10-424-599-23726	Sequence 23726, Appl
17	82.5	8.5	2323	4 US-10-437-963-197361	Sequence 197361, Appl
18	82	8.4	1159	4 US-10-437-963-129387	Sequence 129387, Appl
19	81.5	8.4	304	6 US-11-021-619-22	Sequence 22, Appl
20	81.5	8.4	1959	4 US-10-437-963-154458	Sequence 154458, Appl
21	81.5	8.4	2076	4 US-10-437-963-197291	Sequence 197291, Appl
22	81	8.3	782	6 US-11-097-143-297	Sequence 297, Appl
23	81	8.3	1346	4 US-10-437-963-189131	Sequence 189131, Appl
24	80.5	8.3	538	4 US-10-282-122A-60329	Sequence 60329, Appl
25	80.5	8.3	870	4 US-10-437-963-154457	Sequence 154457, Appl
26	80.5	8.3	1205	4 US-10-437-963-197324	Sequence 197324, Appl
27	80	8.2	270	4 US-10-425-114-56047	Sequence 56047, Appl

28	80	8.2	396	4 US-10-425-114-43995	Sequence 43995, A
29	80	8.2	585	4 US-10-424-599-237273	Sequence 237273, A
30	79.5	8.2	1919	4 US-10-152-886-13	Sequence 13, Appl
31	79.5	8.2	1919	6 US-11-053-576-13	Sequence 13, Appl
32	79.5	8.2	1919	6 US-11-053-576-13	Sequence 13, Appl
33	78.5	8.1	502	4 US-10-108-260A-4245	Sequence 4245, Appl
34	78.5	8.1	912	5 US-10-732-923-6851	Sequence 6851, Appl
35	78.5	8.1	912	5 US-10-732-923-6852	Sequence 6852, Appl
36	78.5	8.1	914	5 US-10-732-923-6854	Sequence 6854, Appl
37	78.5	8.1	965	4 US-10-437-963-160354	Sequence 160354, Appl
38	78.5	8.1	1278	4 US-10-437-963-181016	Sequence 181016, Appl
39	77.5	8.0	937	4 US-10-437-963-197334	Sequence 197334, Appl
40	77.5	8.0	1572	6 US-11-097-143-15396	Sequence 15396, A
41	77	7.9	335	5 US-10-732-923-13080	Sequence 13080, A
42	77	7.9	353	4 US-10-282-122A-74877	Sequence 74877, A
43	77	7.9	400	4 US-10-369-493-12758	Sequence 12758, A
44	77	7.9	457	4 US-10-282-122A-63026	Sequence 63026, A
45	77	7.9	2179	4 US-10-224-999A-3481	Sequence 3481, Appl

ALIGNMENTS

RESULT 1
US-10-627-141-29
Sequence 29, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-627-141-29
Query Match 100.0%; Score 974; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.7e-101;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HTWPSLVFCLIPGLHAAFGVGRSVSTPTTRGGQTVKTAFFYGEKTTORDLT 60

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 32.8167 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974

Sequence: 1 HTVTPSLVFLCLIPGLHAA.....TTIKYLAECMDATLTPV 189

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PTCUR_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfillset.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	100.0	189	2	US-08-779-764A-29
2	974	100.0	189	2	US-09-563-456-29
3	960	98.6	189	2	US-08-779-764A-30
4	960	98.6	189	2	US-09-563-456-30
5	959	98.5	370	2	US-08-369-822C-2
6	959	98.5	370	2	US-08-582-766C-2
7	959	98.5	370	2	US-08-434-831B-2
8	954	97.9	189	2	US-08-779-764A-28
9	954	97.9	189	2	US-09-563-456-28
10	80.5	8.3	568	2	US-09-489-039A-13755
11	79.5	8.2	1919	2	US-10-152-886-13
12	77.5	8.0	409	2	US-09-270-767-42348
13	77.5	7.9	488	2	US-09-540-236-1027
14	76	7.8	534	1	US-08-577-184-2
15	75.5	7.8	346	2	US-09-724-224-6
16	75.5	7.8	346	2	US-10-093-317-6
17	75.5	7.8	370	2	US-09-724-224-2
18	75.5	7.8	370	2	US-10-093-317-2
19	75.5	7.8	487	2	US-09-724-224-8
20	75.5	7.8	487	2	US-10-093-317-8
21	75.5	7.8	490	2	US-09-949-016-8784
22	75.5	7.8	512	2	US-09-724-224-4
23	75.5	7.8	512	2	US-10-093-317-4
24	75.5	7.8	665	2	US-09-595-684B-35
25	75	7.7	761	2	US-09-328-352-5650
26	74.5	7.6	1474	2	US-09-241-606-2
27	74.5	7.6	1474	2	US-09-949-002-287

28	74.5	7.6	1491	2	US-09-949-002-434	Sequence 434, App
29	74	7.6	470	2	US-09-252-991A-25558	Sequence 2558, A
30	73.5	7.5	211	2	US-09-543-681A-6708	Sequence 6708, Ap
31	73	7.5	224	2	US-09-134-000C-3941	Sequence 3941, Ap
32	73	7.5	241	2	US-09-791-540-6	Sequence 6, Appli
33	73	7.5	241	2	US-09-791-578-6	Sequence 6, Appli
34	73	7.5	262	1	US-08-323-445A-4	Sequence 4, Appli
35	73	7.5	262	1	US-08-515-903A-4	Sequence 4, Appli
36	73	7.5	262	4	PCT-US95-12840-4	Sequence 4, Appli
37	73	7.5	264	1	US-08-323-445A-8	Sequence 8, Appli
38	73	7.5	264	1	US-08-515-903A-8	Sequence 8, Appli
39	73	7.5	264	4	PCT-US95-12840-8	Sequence 8, Appli
40	73	7.5	381	1	US-08-687-355A-6	Sequence 6, Appli
41	73	7.5	381	2	US-09-407-367-6	Sequence 6, Appli
42	73	7.5	483	1	US-08-392-388A-19	Sequence 19, Appli
43	73	7.5	483	2	US-09-166-750-19	Sequence 19, Appli
44	73	7.5	483	2	US-09-166-093-19	Sequence 19, Appli
45	73	7.5	483	2	US-09-172-019-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1
US-08-779-764A-29.
Sequence 29, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-764A-29
Query Match 100.0%; Score 974; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.2e-108;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTVTPSLVFLCLIPGLHAAFHGVPRRESYSTPTTGGQTVKTAEPYGEKTTORDLT 60
Db 1 HTVTPSLVFLCLIPGLHAAFHGVPRRESYSTPTTGGQTVKTAEPYGEKTTORDLT 60
QY 61 ELTSSISFGSCSLIGVIVGSSSKIKAEBOIKKKFKTMAAVNPSHGETATLLOMFN 120

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 17, 2006, 15:33:18 ; Search time 18.2315 Seconds

(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974
Sequence: 1 HTWPSLVFCLIPGLHAA.....TTIKVLAECMDATLTIPV 189

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.80:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959	98.5	370	2	A49528
2	82	8.4	1067	2	D96545
3	80	8.2	448	1	A71659
4	80	8.2	908	2	SS1293
5	79.5	8.2	389	1	SVBJCF
6	78.5	8.1	350	2	AC0813
7	78	8.0	408	2	T32237
8	77	7.9	684	2	A82134
9	77	7.9	1252	1	B42771
10	76	7.8	322	1	S31087
11	76	7.8	340	1	C96655
12	75	7.8	497	2	B82721
13	75.5	7.8	200	2	D90133
14	75.5	7.8	311	2	AH2153
15	75.5	7.8	337	2	A10061
16	75.5	7.8	493	2	C71903
17	75.5	7.8	2180	2	A46182
18	75	7.7	216	2	F83051
19	75	7.7	335	2	AB0963
20	75	7.7	620	2	S73809
21	75	7.7	849	2	S77217
22	75	7.7	2123	2	SS5089
23	74.5	7.6	452	2	ER2387
24	74.5	7.6	592	2	ET5032
25	74.5	7.6	803	2	T00092
26	74.5	7.6	920	2	T10052
27	74.5	7.6	1474	1	MAHU
28	74	7.6	427	2	DB3347
29	74	7.6	472	2	B87188

30	74	7.6	507	2	B89792	hypothetical prote
31	74	7.6	678	2	AE0948	probable glycosyl
32	74	7.6	828	2	T12184	probable transcrip
33	74	7.6	857	2	C97707	clpB protein (mpo
34	73.5	7.5	224	1	S74541	negative regulator
35	73.5	7.5	349	2	S71191	thiamin biosynthes
36	73.5	7.5	383	2	H86232	hypothetical prote
37	73.5	7.5	662	2	C54078	hypothetical prote
38	73.5	7.5	872	2	S76197	methy1-accepting c
39	73.5	7.5	889	2	S74173	endopeptidase Clp
40	73	7.5	164	2	C82629	ryanodine receptor
41	73	7.5	233	2	B61222	hypothetical prote
42	73	7.5	315	2	AC2462	cytochrome-c oxida
43	73	7.5	373	2	A86959	two-component resp
44	73	7.5	402	2	AF1929	hypothetical prote
45	73	7.5	1021	2	T42634	hypothetical prote
						connectin/titin -

ALIGNMENTS

RESULT 1

A49528

probable structural component p40 - borna disease virus

N:Alternate names: 39K antigen

C:Species: borna disease virus

C:Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text change 28-Jul-2000

C:Accession: A49528; A37475; S25642; A44004

R:Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A:Title: Sequence conservation in field and experimental isolates of Borna disease virus

A:Reference number: A49528; MUID:94076462; PMID:8254777

A:Accession: A49528

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-370 <SCH>

A:Cross-references: UNIPARC:UPI0000171068; GB:S67502; NID:G456883; PIDN:AA829214.1; PI

A:Experimental source: WT-1, Halle BL/91, horse brain, field isolate

A:Note: Sequence extracted from NCBI backbone (NCBIN:141399, NCBI:141401)

R:Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.R.

Virol. 195, 229-238, 1993

A:Title: Genomic organization of the structural proteins of borna disease virus reveal

A:Reference number: A37475; MUID:93303922; PMID:8317098

A:Accession: A37475

A:Molecule type: mRNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A:Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:G386390; PIDN:AA827261.1; PI

A:Note: Sequence extracted from NCBI backbone (NCBIN:134146, NCBI:134147)

A:Note: parts of this sequence were confirmed by peptide sequencing

R:Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Gredemeyer, O.; Rott, R.; Niemann, S.

Submitted to the EMBL Data Library, September 1992

A:Description: The 39/39K antigen of borna disease virus.

A:Reference number: S25642

A:Accession: S25642

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A:Cross-references: UNIPARC:UPI0000170E05; GB:X68392; NID:G586887; PIDN:CAA8458.1; P

R:McClure, M.A.; Thibault, K.J.; Hatalaki, C.G.; Lipkin, W.I.

J. Virol. 66, 6572-6577, 1992

A:Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w

A:Reference number: A44004; MUID:93021385; PMID:1404604

A:Accession: A44004

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 14-46, 'T', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A:Cross-references: UNIPARC:UPI0000170E06; GB:M99375; NID:G210658; PIDN:AAA73385.1; PI

C:Superfamily: Borna disease virus p40

Query Match 98.5%; Score 959; DB 2; Length 370;

Best Local Similarity 97.9%; Pred. No. 9.5e-63;

Matches 185; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 / Search time 125.19 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974

Sequence: 1 HTVPSLVPLCLRLPGHAA.....TTIKYLAECMDATLTIPV 189

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	100.0	189	2	AAW49052 Human Bor
2	960	98.6	189	2	AAW49053 Human Bor
3	959	98.5	370	2	AAW49051 Human Bor
4	954	97.9	189	2	AAW49051 Human Bor
5	329.5	33.8	273	4	AAW42095 Human pol
6	329.5	33.8	273	7	ADB09066 Human pol
7	329.5	33.8	273	7	ADB09066 Human pol
8	323.5	33.2	541	8	ADN99838 Novel hum
9	323.5	33.2	541	8	ADN99838 Novel hum
10	316	32.4	208	4	AAW40309 Human pol
11	316	32.4	208	4	AAW40309 Human pol
12	312	32.0	272	7	ADB08030 Novel pro
13	312	32.0	272	7	ADB08030 Novel pro
14	141.5	14.5	85	3	AAW42995 Human ORF
15	93	9.5	90	3	AAW43320 Human ORF
16	86.5	8.9	988	7	ADM27076 Hypertether
17	85	8.7	82	4	AAW42029 Human hae
18	84.5	8.7	2225	4	ABW71877 Drosophila
19	82	8.4	1067	5	ABW71877 Drosophila
20	81.5	8.4	304	9	ABW71877 Drosophila
21	81.5	8.4	1125	8	ADN46700 Thermococ
22	81	8.3	782	4	ABW57835 Drosophila
23	80.5	8.3	538	6	ABW57835 Drosophila
24	80.5	8.3	568	7	ABW57835 Drosophila

25	80	8.2	270	8	ADX93383 Plant ful
26	80	8.2	395	8	ADY74629 Plant ful
27	79.5	8.2	1919	5	ABG97422 M. echino
28	79.5	8.2	1919	9	ABE12617 Eneidiyne
29	79.5	8.2	1919	9	ABE12617 Eneidiyne
30	78.5	8.1	502	7	ADM05560 Human pro
31	77.5	8.0	468	5	ADP26705 Streptococ
32	77.5	8.0	592	8	ADW46285 Thermococ
33	77.5	8.0	1572	4	ABB62868 Drosophila
34	77	7.9	353	6	ABU46953 Protein e
35	77	7.9	400	8	ADW23725 Bacterial
36	77	7.9	457	6	ABU35102 Protein e
37	77	7.9	488	8	ADL05341 M. catarr
38	77	7.9	1254	2	AAW07503 Merozoite
39	77	7.9	1254	2	AAW24575 Merozoite
40	77	7.9	2179	7	ADJ92013 Human par
41	76.5	7.9	266	2	AAW61333 Human pot
42	76.5	7.9	1719	4	ABW70837 Drosophila
43	76	7.8	322	3	AAW39031 Arabidops
44	76	7.8	534	2	AAW39031 Arabidops
45	76	7.8	534	2	AAW13273 Rhodococc

ALIGNMENTS

RESULT 1
ID AAW49052 standard; protein, 189 AA.
XX
XX AAW49052;
XX
XX 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
DT
XX
DE Human Borna disease virus p40 polypeptide.
XX
XX BDV; infection; diagnosis; neuropsychiatric disorder; human.
XX
XX Borna disease virus.
OS
XX
XX W09830238-A1.
XX
XX 16-JUL-1998.
XX
XX 07-JAN-1998; 98WO-US000495.
XX
XX 07-JAN-1997; 97US-00779764.
XX
XX (SCRI) SCRIIPS RES INST.
XX
XX De La Torre JC;
XX
XX WPI; 1998-398802/34.
XX
XX N-PSDB; AAW32852.
XX
XX New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.
XX
XX Claim 12; Fig 11B; 207pp; English.
XX
XX This is the p40 polypeptide of a Borna disease virus (BDV) isolate, designated H2, that was obtained from a psychiatric patient with a mood disorder. Nucleic acids (see AAW32840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain polypeptides (see AAW39043-63) are provided. These have been obtained from 3 psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV polypeptides. Human BDV polypeptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 117.593 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HTWPSLVPLCLIPGLHAA.....TTIKYLAECMDATLTIPV 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main: *
1: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/us10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/us10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	978	100.0	189	4 US-10-627-141-28	Sequence 28, Appl
2	969	99.1	189	4 US-10-627-141-30	Sequence 30, Appl
3	954	97.5	189	4 US-10-627-141-29	Sequence 29, Appl
4	327.5	53.5	273	5 US-10-128-558-370	Sequence 370, Appl
5	310	31.7	272	5 US-10-128-558-185	Sequence 185, Appl
6	89	9.1	238	4 US-10-291-190-25	Sequence 25, Appl
7	88.5	9.0	940	4 US-10-437-963-197289	Sequence 197289, Appl
8	88.5	9.0	1350	4 US-10-437-963-125423	Sequence 125423, Appl
9	88.5	9.0	2225	6 US-11-097-143-42423	Sequence 42423, Appl
10	86	8.8	82	3 US-09-796-692-2393	Sequence 2393, Appl
11	86	8.8	82	4 US-10-040-862-6393	Sequence 2393, Appl
12	86	8.8	82	4 US-10-057-4758-2393	Sequence 2393, Appl
13	86	8.8	82	4 US-10-154-8848-2393	Sequence 2393, Appl
14	86	8.8	82	4 US-10-764-324-2393	Sequence 2393, Appl
15	85	8.7	139	4 US-10-424-599-237276	Sequence 237276, Appl
16	84.5	8.6	1186	4 US-10-437-963-197319	Sequence 197319, Appl
17	83.5	8.5	304	6 US-11-021-619-22	Sequence 22, Appl
18	82	8.4	270	4 US-10-425-114-56047	Sequence 56047, Appl
19	82	8.4	336	4 US-10-425-114-43995	Sequence 43995, Appl
20	82	8.4	439	4 US-10-282-122A-50928	Sequence 50928, Appl
21	82	8.4	585	4 US-10-434-599-237273	Sequence 237273, Appl
22	80.5	8.2	1190	6 US-11-087-143-14232	Sequence 14232, Appl
23	79.5	8.1	1919	4 US-10-152-886-13	Sequence 13, Appl
24	79.5	8.1	1919	6 US-11-053-576-13	Sequence 13, Appl
25	79.5	8.1	1919	6 US-11-053-052-13	Sequence 13, Appl
26	79	8.1	782	6 US-11-097-143-297	Sequence 297, Appl
27	79	8.1	1159	4 US-10-437-963-129387	Sequence 129387, Appl

28	77.5	7.9	1959	4 US-10-437-963-154458	Sequence 154458, Appl
29	77.5	7.9	2076	4 US-10-437-963-197291	Sequence 197291, Appl
30	77	7.9	420	4 US-10-094-749-2235	Sequence 2235, Appl
31	77	7.9	481	3 US-09-955-999-104	Sequence 104, Appl
32	77	7.9	847	4 US-10-478-245-7	Sequence 189131, Appl
33	77	7.9	1346	4 US-10-437-963-189131	Sequence 189131, Appl
34	76.5	7.8	246	3 US-09-880-748-1393	Sequence 1393, Appl
35	76.5	7.8	246	4 US-10-293-418-1393	Sequence 1393, Appl
36	76.5	7.8	249	3 US-09-880-748-1347	Sequence 1347, Appl
37	76.5	7.8	249	4 US-10-293-418-1347	Sequence 1347, Appl
38	76.5	7.8	447	4 US-10-282-122A-48992	Sequence 48992, Appl
39	76.5	7.8	870	4 US-10-437-963-154457	Sequence 154457, Appl
40	76.5	7.8	1205	4 US-10-437-963-197324	Sequence 197324, Appl
41	76.5	7.8	1563	4 US-10-437-963-190562	Sequence 190562, Appl
42	76	7.8	353	4 US-10-282-122A-74877	Sequence 74877, Appl
43	76	7.8	527	4 US-10-369-493-12758	Sequence 12758, Appl
44	76	7.8	527	4 US-10-437-963-203871	Sequence 203871, Appl
45	75.5	7.7	400	4 US-10-335-977-5588	Sequence 5588, Appl

ALIGNMENTS

RESULT 1
US-10-627-141-28
Sequence 28, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESSES:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitching, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-627-141-28
Query Match 100.0%; Score 978; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e-103;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HTWPSLVPLCLIPGLHAAFYGVGVRSYVSTPVRGQVTKRAFGKGTQORDLT 60
|||||

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 32.8167 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HTVPSLVFLCLIPGLHAFA.....TIKEYLAECMDATLTPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:*
4: /cgn2_6/prodata/1/1aa/PCUS COMB.pep:*
5: /cgn2_6/prodata/1/1aa/RE COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	189	2 US-08-779-764A-28	Sequence 28, Appl
2	978	100.0	189	2 US-09-563-456-28	Sequence 28, Appl
3	970	99.2	370	2 US-08-369-822C-2	Sequence 2, Appl
4	970	99.2	370	2 US-08-582-776C-2	Sequence 2, Appl
5	970	99.2	370	2 US-08-434-831B-2	Sequence 2, Appl
6	969	99.1	189	2 US-08-779-764A-30	Sequence 30, Appl
7	969	99.1	189	2 US-09-563-456-30	Sequence 30, Appl
8	954	97.5	189	2 US-08-779-764A-29	Sequence 29, Appl
9	954	97.5	189	2 US-09-563-456-29	Sequence 29, Appl
10	79.5	8.1	1919	2 US-10-152-886-13	Sequence 29, Appl
11	76	7.8	534	1 US-08-577-184-2	Sequence 13, Appl
12	75	7.7	761	2 US-09-328-352-5650	Sequence 4482, Ap
13	74.5	7.6	519	2 US-09-134-000C-4482	Sequence 7, Appl
14	74	7.6	404	2 US-08-459-953A-7	Sequence 9804, Ap
15	74	7.6	404	2 US-09-393-212-7	Sequence 42348, A
16	74	7.6	978	2 US-09-949-016-9804	Sequence 9859, Ap
17	73.5	7.5	409	2 US-09-270-767-42348	Sequence 636, App
18	73	7.5	797	2 US-09-949-016-9859	Sequence 596, App
19	73	7.5	814	2 US-09-198-452A-636	Sequence 2, Appl
20	73	7.5	814	2 US-09-438-185A-596	Sequence 2, Appl
21	72.5	7.4	393	2 US-08-459-953A-2	Sequence 14220, A
22	72.5	7.4	393	2 US-09-393-212-2	Sequence 14220, A
23	72.5	7.4	859	2 US-09-302-540-14220	Sequence 24, Appl
24	72.5	7.4	885	2 US-09-342-648-9	Sequence 24, Appl
25	72	7.4	367	2 US-09-025-580-24	Sequence 25558, A
26	72	7.4	367	2 US-09-642-749-24	
27	72	7.4	470	2 US-09-252-991A-25558	

28	71.5	7.3	211	2 US-09-543-681A-6708	Sequence 6708, Ap
29	71.5	7.3	1474	2 US-09-241-606-2	Sequence 2, Appl
30	71.5	7.3	1474	2 US-09-949-002-287	Sequence 287, App
31	71.5	7.3	1491	2 US-09-949-002-434	Sequence 434, App
32	71.5	7.3	1721	2 US-10-042-665A-6	Sequence 6, Appl
33	71	7.3	367	2 US-09-457-040B-1	Sequence 1, Appl
34	71	7.3	367	2 US-09-457-040B-33	Sequence 33, Appl
35	71	7.3	367	2 US-09-538-092-1203	Sequence 103, Ap
36	71	7.3	488	2 US-09-540-236-3027	Sequence 3027, Ap
37	70.5	7.2	352	2 US-09-270-767-41652	Sequence 41652, A
38	70.5	7.2	427	2 US-09-489-039A-12852	Sequence 12852, A
39	70.5	7.2	440	2 US-09-591-095-27	Sequence 27, Appl
40	70.5	7.2	456	2 US-09-949-016-9294	Sequence 9294, Ap
41	70.5	7.2	568	2 US-09-489-039A-13755	Sequence 13755, A
42	69.5	7.1	455	2 US-09-328-352-4555	Sequence 4555, Ap
43	69.5	7.1	919	2 US-09-919-039-222	Sequence 222, App
44	69.5	7.1	1219	2 US-09-107-532A-6020	Sequence 6020, Ap
45	69	7.1	151	2 US-09-710-279-1646	Sequence 1646, Ap

ALIGNMENTS

RESULT 1
US-08-779-764A-28
Sequence 28, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
City: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-779-764A-28
Query Match 100.0%; Score 978; DB 2; Length 189;
Best local Similarity 100.0%; Pred. No. 4.6e-111;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTVPSLVFLCLIPGLHAFAFHGVGVPRESYSTPTVRSBQIVVKTAKYGGKTTORDLT 60
DB 1 HTVPSLVFLCLIPGLHAFAFHGVGVPRESYSTPTVRSBQIVVKTAKYGGKTTORDLT 60
QY 61 EIEISSIFHCSSILIGVYIGSSSKTAKAGADIKKFKTMALNPSHGETTLLQWNT 120

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 18.2315 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978

Sequence: 1 HTVTPSLVFLCLIPGLHAA.....TTIKXYLAEGMDATLTPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:.*
2: PIR:.*
3: PIR:.*
4: PIR:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	970	99.2	370	2	A49528	Probable structural
2	85	8.7	448	1	A71659	DNA repair protein
3	81.5	8.3	311	2	AH2153	hypothetical prote
4	81	8.3	388	2	T36766	probable two-compo
5	81	8.3	1224	2	T19749	hypothetical prote
6	80.5	8.2	200	2	C41873	heat shock protein
7	80.5	8.2	200	2	A97058	molecular chaperon
8	77.5	7.9	332	2	T34758	oligopeptide trans
9	77.5	7.9	675	2	S16625	penicillin-binding
10	77	7.9	408	2	T32237	hypothetical prote
11	77	7.9	666	2	S54401	penicillin-binding
12	77	7.9	1021	2	T42634	connectin/citin
13	76.5	7.8	180	1	FXAVEP	flavodoxin - Azoto
14	76.5	7.8	303	2	AB1937	hypothetical prote
15	76.5	7.8	350	2	AC0813	ethanolamine oporo
16	76.5	7.8	592	2	E75032	carbon starvation
17	76	7.8	1252	2	B42771	reticulocyte-bind
18	75.5	7.7	337	2	A10061	hypothetical prote
19	75.5	7.7	389	1	SYFUCF	naringenin-chalcon
20	75.5	7.7	493	1	C71903	D-alanyl-D-alanine
21	75.5	7.7	1303	1	S27396	phytochrome / prot
22	75	7.7	620	2	S73809	DNA primase - Myco
23	75	7.7	792	2	G86564	phenylalanyl tRNA
24	75	7.7	849	2	S77217	phosphorylase (EC
25	75	7.7	2133	2	S55089	probable acetyl-Co
26	74	7.6	388	2	B61222	cytochrome-c oxida
27	74	7.6	333	2	F75162	tryptophan synthas
28	73.5	7.5	352	2	A69743	ATP-binding Msp-1i
29	73.5	7.5	383	2	H86232	hypothetical prote

30	73.5	7.5	457	2	G82187	biopolymer transpo
31	73.5	7.5	920	2	T10052	aminopeptidase (EC
32	73	7.5	792	2	H72058	phenylalanine-tRNA
33	73	7.5	792	2	D81608	phenylalanine-tRNA
34	73	7.5	908	2	S51293	probable membrane
35	73	7.5	1333	2	S65812	RNA-directed DNA p
36	72.5	7.4	248	2	S33756	granzyme-like prot
37	72.5	7.4	37	2	C72276	phosphatase ABC tran
38	72.5	7.4	329	2	H71192	hypothetical prote
39	72.5	7.4	885	2	I38968	100 kDa coactivator
40	72	7.4	335	2	AB0983	probable lact-fami
41	72	7.4	351	2	T29369	hypothetical prote
42	72	7.4	427	2	D83347	probable aminotran
43	71.5	7.3	300	2	AE1723	ABC transporter (A
44	71.5	7.3	433	2	S05654	ND3 intron protein
45	71.5	7.3	662	2	C54078	methyl-accepting c

ALIGNMENTS

RESULT 1

A49528

probable structural component p40 - borna disease virus

N:Alternate names: 39k antigen

C:Species: borna disease virus

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000

C/Accession: A49528; A37475; S25642; A44004

R:Schneider, P.A.; Briese, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A>Title: Sequence conservation in field and experimental isolates of Borna disease virus

A/Reference number: A49528; PMID:94076462; PMID:8254777

A/Accession: A49528

A/Status: preliminary

A/Molecule type: genomic RNA

A/Cross-references: UNIPARC:UPI00001708E; GB:67502; NID:G3686390; PIDD:AMB27261.1; PII

A/Experimental source: WT-1, Halle B1/91, horse brain, field isolate

R:Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A>Title: Genomic organization of the structural proteins of borna disease virus reveal

A/Reference number: A37475; PMID:93303922; PMID:8317098

A/Accession: S25642

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A/Cross-references: UNIPARC:UPI00001708E5; GB:S62821; NID:G3686390; PIDD:AMB27261.1; PII

A/Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBIPI:134147)

A/Note: parts of this sequence were confirmed by peptide sequencing

R:Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A/Description: The 39/39k antigen of borna disease virus.

A/Reference number: S25642

A/Accession: S25642

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A/Cross-references: UNIPARC:UPI00001708E6; GB:M93975; NID:G210698; PIDD:AAA73385.1; PII

C/Superfamily: borna disease virus p40

Query Match 99.2% Score 970; DB 2; Length 370;

Best Local Similarity 99.5% Pred. No. 1.2e-84;

Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:48:14 ; Search time 22.1817 seconds
(without alignments)
348.754 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HTVPSLWFLCLIPGLHAA.....TTIKYLAECMDATLIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 150911 seqs, 40930936 residues

Total number of hits satisfying chosen parameters: 150911

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/2/paa/PCY NEW COMB pep:*
2: /cgn2_6/ptodata/2/paa/US06 NEW COMB pep:*
3: /cgn2_6/ptodata/2/paa/US07 NEW COMB pep:*
4: /cgn2_6/ptodata/2/paa/US08 NEW COMB pep:*
5: /cgn2_6/ptodata/2/paa/US09 NEW COMB pep:*
6: /cgn2_6/ptodata/2/paa/US10 NEW COMB pep:*
7: /cgn2_6/ptodata/2/paa/US11 NEW COMB pep:*
8: /cgn2_6/ptodata/2/paa/US60 NEW COMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.5	7.9	1574	US-11-268-554-114	Sequence 114, App
2	77	7.9	847	US-60-742-219-298	Sequence 298, App
3	77	7.9	889	US-60-742-219-300	Sequence 300, App
4	76.5	7.8	246	US-11-266-444-1393	Sequence 1393, App
5	76.5	7.8	246	US-60-735-988-1393	Sequence 1393, App
6	76.5	7.8	249	US-11-266-444-1347	Sequence 1347, App
7	76.5	7.8	249	US-60-735-988-1347	Sequence 1347, App
8	74	7.6	251	US-11-266-444-1669	Sequence 1669, App
9	74	7.6	251	US-60-735-988-1669	Sequence 1669, App
10	74	7.6	1033	US-10-276-817B-14850	Sequence 14850, A
11	74	7.6	1428	US-11-299-791-22	Sequence 22, App1
12	73.5	7.5	3173	US-10-558-119-223	Sequence 223, App
13	73	7.5	472	US-10-276-817B-13919	Sequence 13919, A
14	73	7.5	908	US-60-752-355-12907	Sequence 12907, A
15	72.5	7.4	633	US-60-741-048-47	Sequence 47, App1
16	72.5	7.4	910	US-60-741-048-46	Sequence 46, App1
17	71.5	7.3	485	US-11-311-940-1123	Sequence 1123, App
18	71.5	7.3	506	US-11-311-940-4063	Sequence 4063, App
19	71.5	7.3	1474	US-60-741-051-104	Sequence 104, App
20	71.5	7.3	1474	US-60-741-051-105	Sequence 105, App1
21	71	7.3	367	US-11-303-901-10	Sequence 10, App1
22	70.5	7.2	375	US-11-311-940-414	Sequence 414, App
23	70.5	7.2	753	US-60-752-355-3310	Sequence 3310, App
24	70	7.2	475	US-60-752-355-27866	Sequence 27866, A
25	69.5	7.1	396	US-11-311-940-3786	Sequence 3786, App

26	69.5	7.1	733	US-11-311-940-6017	Sequence 6017, App
27	69.5	7.1	753	US-60-752-355-32717	Sequence 32717, A
28	69.5	7.1	875	US-11-289-102-364	Sequence 364, App
29	69	7.1	315	US-60-752-355-30760	Sequence 30760, A
30	69	7.1	315	US-60-752-355-46410	Sequence 46410, A
31	69	7.1	510	US-10-558-119-447	Sequence 447, App
32	68.5	7.0	338	US-60-752-355-32869	Sequence 32869, A
33	68.5	7.0	358	US-60-752-355-29675	Sequence 29675, A
34	68.5	7.0	533	US-60-752-355-21538	Sequence 21538, A
35	68.5	7.0	613	US-60-752-355-35535	Sequence 35535, A
36	68.5	7.0	629	US-10-868-184C-4170	Sequence 4170, App
37	68.5	7.0	634	US-11-311-940-3999	Sequence 3999, App
38	68.5	7.0	753	US-60-752-355-7910	Sequence 7910, App
39	68.5	7.0	753	US-60-752-355-30529	Sequence 30529, A
40	68.5	7.0	753	US-60-752-355-36523	Sequence 36523, A
41	68.5	7.0	1033	US-10-501-841-15	Sequence 15, App1
42	68.5	7.0	3343	US-11-122-396-7	Sequence 7, App1
43	68	7.0	537	US-11-246-765A-72	Sequence 72, App1
44	68	7.0	582	US-60-752-355-18475	Sequence 18475, A
45	67.5	6.9	249	US-11-266-444-1296	Sequence 1296, App

ALIGNMENTS

```

RESULT 1
US-11-268-554-114
; Sequence 114, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; FILE REFERENCE: C0001557
; CURRENT APPLICATION NUMBER: US/11/268, 554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-268-554-114

Query Match      7.9%; Score 77.5; DB 7; Length 1574;
Best Local Similarity 26.6%; Pred. No. 5.8;
Matches 38; Conservative 14; Mismatches 74; Indels 17; Gaps 5;

Cy 15 PGLAARVHGVPRESYISTPTVTRGEQTV-KTAKFYGKTKYQDRLTELSISPSHCS 73
Db 1162 PYAHICPLHNSKTEIHSITLNPWTQITIFDEVEIYGEPTVLQNPVKVIMELFDN--- 1218
Cy 74 LLIGVIGSSSKI---KAGAEQIKRFRKMMALNRPESHGETATLQWPNHBAIDWING 130
Db 1219 ---DQVQGNKILHQLGAPERLALHILATQGLVBEHVTITLHSTFGPN--ISQKL 1273
Cy 131 QPWGSGFVLPLLTDTDFSPCKEF 153
Db 1274 QMWVDVPPKSL-----GPPGPPF 1291

RESULT 2
US-60-742-219-298
; Sequence 298, Application US/60742219
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John Vermer
; APPLICANT: Bradley, Walter Edward
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall David
; APPLICANT: Keith, Tim

```


GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds

(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978

Sequence: 1 HVTPLSLVFLCLIPGLHA.....TTIKYLAECMDATLTIPV 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_05.80:*

2: uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	190	2	065468_BDV
2	970	99.2	370	1	VP40_BDV
3	970	99.2	370	2	010395_BDV
4	970	99.2	370	2	010401_BDV
5	970	99.2	370	2	05GL86_BDV
6	970	99.2	370	2	05GL92_BDV
7	970	99.2	370	2	05GL95_BDV
8	970	99.2	370	2	05GL98_BDV
9	970	99.2	370	2	05GLD1_BDV
10	970	99.2	370	2	08B829_BDV
11	970	99.2	370	2	0910H1_BDV
12	970	99.2	370	2	091U41_BDV
13	970	99.2	370	2	091U48_BDV
14	970	99.2	370	2	0774E9_BDV
15	969	99.1	190	2	065470_BDV
16	969	99.1	370	2	010398_BDV
17	966	98.8	370	2	05GL50_BDV
18	964	98.6	370	2	05GL62_BDV
19	964	98.6	370	2	05GL71_BDV
20	964	98.6	370	2	05GL83_BDV
21	963	98.5	369	2	09G9V1_BDV
22	960	98.2	370	2	010392_BDV
23	954	97.5	190	2	065469_BDV
24	954	97.5	176	2	077A29_BDV
25	904	92.4	176	2	077A30_BDV
26	904	92.4	176	2	077A31_BDV
27	904	92.4	176	2	077A32_BDV
28	904	92.4	176	2	077A33_BDV
29	904	92.4	176	2	077A34_BDV
30	904	92.4	176	2	09WB22_BDV
31	904	92.4	176	2	09WB22_BDV

32	890	91.0	176	2	09WN17_BDV	09WN17_BDV
33	778	79.6	152	2	09GCJ2_BDV	09GCJ2_BDV
34	751	76.8	146	2	012852_BDV	012852_BDV
35	751	76.8	146	2	012853_BDV	012853_BDV
36	751	76.8	146	2	012855_BDV	012855_BDV
37	751	76.8	146	2	012856_BDV	012856_BDV
38	751	76.8	146	2	012857_BDV	012857_BDV
39	751	76.8	146	2	012858_BDV	012858_BDV
40	751	76.8	146	2	012859_BDV	012859_BDV
41	751	76.8	146	2	012860_BDV	012860_BDV
42	751	76.8	146	2	012861_BDV	012861_BDV
43	751	76.8	146	2	012862_BDV	012862_BDV
44	751	76.8	146	2	012863_BDV	012863_BDV
45	751	76.8	146	2	012864_BDV	012864_BDV

ALIGNMENTS

RESULT 1	065468_BDV	PRELIMINARY;	PRT;	190 AA.
ID	065468_BDV	PRELIMINARY;	PRT;	190 AA.
AC	065468;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DS	P40 (Fragment).			
OS	Borna disease virus (BDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;			
OX	Bornavirus.			
NC	NCBI_TaxID=12455;			
RP	NCBI_TaxID=12455;			
RN	NUCLEOTIDE SEQUENCE.			
RA	MEDLINE=97233300; PubMed=9118344;			
RX	Bode L., Duerwald R., Rantam F.A., Ferszt R., Ludwig H.;			
RT	"First isolates of infectious human Borna disease virus from patients with mood disorders."			
RL	Mol. Psychiatry 1:200-212 (1996).			
DR	EMBL; U58594; AAB05242.1; -; Genomic_RNA.			
DR	HSSP; 001552; IN93.			
DR	InterPro; IPR009441; BDV_P40.			
DR	PANTHER; PTHR10207; BDV_P40; 1.			
DR	Pfam; PF06407; BDV_P40; 1.			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	190 AA; 20896 MW; 75FCA8B1370BB9C CRC64;		
Query Match	100.0%; Score 978; DB 2; Length 190;			
Best Local Similarity	100.0%; Pred. No. 1.1e-86;			
Matches 189; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1 HVTPLSLVFLCLIPGLHAFAVHGVPRESYSTPTVRGQVAVAKFGKTTORDLT 60			
DB	1 HVTPLSLVFLCLIPGLHAFAVHGVPRESYSTPTVRGQVAVAKFGKTTORDLT 60			
QY	61 EHEISIFSHCCSLIGVIGSSSKIKAGABQIKKFKTMALNRPSEGETATLLQMFN 120			
DB	61 EHEISIFSHCCSLIGVIGSSSKIKAGABQIKKFKTMALNRPSEGETATLLQMFN 120			
QY	121 PHEAIDWINGQPMWGSFVPLPLTTDFESPKEFMQIKIVASYAQMVTYTTIKYLAECM 180			
DB	121 PHEAIDWINGQPMWGSFVPLPLTTDFESPKEFMQIKIVASYAQMVTYTTIKYLAECM 180			
QY	181 DATLTIPV 189			
DB	181 DATLTIPV 189			
RESULT 2	VP40_BDV	STANDARD;	PRT;	370 AA.
ID	VP40_BDV	STANDARD;	PRT;	370 AA.
AC	001552;			
DT	01-JUL-1993 (rel. 26, Created)			